

GenCore version 4.5
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CM protein - protein search, using sw model

Run on: December 13, 1999, 02:19:50 ; Search time 29.27 Seconds

(without alignments)
323.691 Million cell updates/sec

Title: US-09-272-835-15
Perfect score: 2190

Sequence: 1 MVRPLNPRLPVPVLMILL.....PMVPSLSCTLPILLLSIM 400

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Abase: A_Geneseq_36.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2190	100.0	400 1	Human Ret ligand R
2	2190	100.0	400 1	Human GDNF alpha-3
3	2190	100.0	400 1	Glial cell line-de
4	2186	99.8	400 1	A GDNF-alpha-rela
5	2184	99.7	400 1	Human GDNF alpha-3
6	2043	93.3	378 1	Glial cell line-de
7	1708	78.0	315 1	Human Ret ligand R
8	1646.5	75.2	397 1	Mouse Ret ligand R
9	1642.5	75.0	397 1	A GDNF-alpha-rela
10	1455	66.4	346 1	Mouse Ret ligand R
11	944	43.1	172 1	Human GDNF alpha-3
12	632.5	28.9	498 1	Human GDNF alpha-3
13	589.5	26.9	489 1	Consensus sequence
14	547.5	25.0	460 1	A GDNF-alpha-rela
15	544.5	24.9	463 1	Mouse Ret ligand R
16	544.5	24.9	411 1	Mouse mature TGF-beta
17	542.5	24.8	664 1	Rat mature TGF-beta
18	542.5	24.8	664 1	Rat neurturin rece
19	542.5	24.8	464 1	Rat neurturin rece
20	540.5	24.7	464 1	Human Ret ligand R
21	540.5	24.7	464 1	Human Ret ligand R
22	540.5	24.7	464 1	Human Ret ligand R
23	540.5	24.7	464 1	Human Ret ligand R
24	540.5	24.7	464 1	Human Ret ligand R
25	540.5	24.7	464 1	Human Ret ligand R
26	540.5	24.7	464 1	Human Ret ligand R
27	540.5	24.7	464 1	Human Ret ligand R
28	517.5	23.6	460 1	Human Ret ligand R
29	516	23.6	465 1	Human Ret ligand R
30	516	23.6	465 1	Human Ret ligand R
31	516	23.6	463 1	Human Ret ligand R
32	516	23.6	463 1	Human Ret ligand R
33	516	23.6	465 1	Human Ret ligand R
34	515	23.5	465 1	Human Ret ligand R
35	511	23.3	468 1	Human Ret ligand R
36	511	23.3	468 1	Human Ret ligand R
37	511	23.3	468 1	Human Ret ligand R
38	511	23.3	468 1	Human Ret ligand R
39	504	23.0	468 1	Human Ret ligand R
40	405	18.5	330 1	Human Ret ligand R
41	401	18.3	331 1	Human Ret ligand R
42	389.5	17.8	346 1	Human Ret ligand R
43	336.5	15.4	232 1	Human Ret ligand R

ALIGNMENTS

RESULT 1
ID W37463 standard; Protein; 400 AA.
AC W37463;
DE 21-MAY-1998 (first entry)
KW Human Ret ligand Ret3.
KW Ret ligand; Ret3; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Homo sapiens.
PN M09744336-A2
PF 07-MAY-1997; U07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (Bio) BIOGEN INC.
PI Cate RL, Hession C, Sanicola-Nadel M;
W37463-01831/02;
DR N-PSDB; V00251.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT -vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 2: Page 85-86; 113p; English.
CC This amino acid sequence comprises human Ret ligand (Ret), Ret3,
CC deduced from cDNA clones (see V00251) isolated from a adult heart
CC and spinal cord libraries. Rat and human Ret3, human Ret2 and
CC mouse Ret3 sequences (see W37457-62) are also claimed. Human
CC Ret3 is 34.3% identical to human Ret3, 34.9% identical to human
CC Ret2 and 76.8% identical to murine Ret3. Ret ligand is a key
CC component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret dimetrisation
CC and/or autophosphorylation of the Ret tyrosine kinase domain.
CC Vectors containing Ret3 DNA and prokaryotic or eukaryotic host
CC cells transfected or transfected with these vectors are claimed, as
CC well as a method for production of Ret3. Its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC Ret3, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
CC associated with HIV or prion infections (e.g. meningitis, myelopathy
CC or spinal cord injury, developmental disorders such as Down's syndrome
CC and cerebral palsy, or conditions involving the peripheral nervous
CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
CC cells, especially tumours.
SQ Sequence 400 AA.

Query Match 100.0%; Score 2190; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.8e-188;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MVRPLNPRLPVPVLMILLIPSPPLAAGDPLTESRLMNSCLARRKCAADPTCSAA 60
1 MVRPLNPRLPVPVLMILLIPSPPLAAGDPLTESRLMNSCLARRKCAADPTCSAA 60

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QY 61 YHLDSCSTSSITPLPSEEPSVPADCLEAAOOLRNSSLIGCMCHRRMKNOVACLDIYTWY 120
DB 61 YHLDSCSTSSITPLPSEEPSVPADCLEAAOOLRNSSLIGCMCHRRMKNOVACLDIYTWY 120
QY 121 HRAISIGNELDVSPYEDVTSKPMKMNLSKLNMLKPPSDCLCFKFMCTLNDKCDRLRK 180
DB 121 HRAISIGNELDVSPYEDVTSKPMKMNLSKLNMLKPPSDCLCFKFMCTLNDKCDRLRK 180
QY 181 AYGEACSGPHCGHVCRLQLLTFFEKAAEPHAGLLCPAPNDRCGERRRNTIAPNCA 240
DB 181 AYGEACSGPHCGHVCRLQLLTFFEKAAEPHAGLLCPAPNDRCGERRRNTIAPNCA 240
QY 241 LPVPANCLERLRCFSDPLCRSLVDFTCHHPMDILGTCATEOSRCLRAYIGLIGTAM 300
DB 241 LPVPANCLERLRCFSDPLCRSLVDFTCHHPMDILGTCATEOSRCLRAYIGLIGTAM 300
QY 301 TPNEFVSNTSVALSCTCRGSGNLQECCEMTEGFFSHNPCLTEAIAAKRRHSOLFSDQM 360
DB 301 TPNEFVSNTSVALSCTCRGSGNLQECCEMTEGFFSHNPCLTEAIAAKRRHSOLFSDQM 360
QY 361 PPHTEFAVAHONENPAVRPOPWPVPSLFCSTLPLILLISLM 400
DB 361 PPHTEFAVAHONENPAVRPOPWPVPSLFCSTLPLILLISLM 400

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RESULT 2
ID W65116
AC W65116;
DE 28-SEP-1998 (first entry)
DE Human GDNF alpha-3 receptor protein #1.
KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
KW treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
KW Huntington's disease; Alzheimer's disease; diabetic neuropathy; muscle;
KW muscular dystrophy; diagnostic.
OS Homo sapiens.
FH Key
FT Location/Qualifiers
FT 1..400
FT /label= "GDNF alpha-3
FT /note= "Partial sequence"
PD EP-846764-A2.
PD 10-SEP-1998
PD 20-NOV-1997; 309375.
PE 09-MAY-1997; GB-009463.
PR 27-NOV-1996; GB-024677.
PR (SMK) SMITHKLINE BEECHAM PLC.
PA Lawrence GMP;
WPI: 98-299980/27.
N-PSDB: V35364.
DR New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
PT used to treat neuro degenerative diseases, muscular diseases and
PT nerve and muscle trauma and in diagnostic assays
PS Claim 4; Fig 2; 22pp; English.
CC This sequence represents a novel glial cell line-derived neurotrophic
CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to
CC treat e.g. neurodegenerative diseases (such as Parkinson's disease,
CC amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA),
CC Huntington's disease, Alzheimer's disease, diabetic neuropathy),
CC muscular diseases (including the muscular dystrophies) and nerve and
CC muscle trauma and in diagnostic assays for such conditions.
SQ Sequence 400 AA;

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Query Match 100.0%; Score 2190; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.8e-188;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYRPLNPRPLRPVYVIMLLPLPSPLPLAAGDPLTERLNKSCIQARRKKQADPTCSAA 60
DB 1 MYRPLNPRPLRPVYVIMLLPLPSPLPLAAGDPLTERLNKSCIQARRKKQADPTCSAA 60

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QY 61 YHLDSCSTSSITPLPSEEPSVPADCLEAAOOLRNSSLIGCMCHRRMKNOVACLDIYTWY 120
DB 61 YHLDSCSTSSITPLPSEEPSVPADCLEAAOOLRNSSLIGCMCHRRMKNOVACLDIYTWY 120
QY 121 HRAISIGNELDVSPYEDVTSKPMKMNLSKLNMLKPPSDCLCFKFMCTLNDKCDRLRK 180
DB 121 HRAISIGNELDVSPYEDVTSKPMKMNLSKLNMLKPPSDCLCFKFMCTLNDKCDRLRK 180
QY 181 AYGEACSGPHCGHVCRLQLLTFFEKAAEPHAGLLCPAPNDRCGERRRNTIAPNCA 240
DB 181 AYGEACSGPHCGHVCRLQLLTFFEKAAEPHAGLLCPAPNDRCGERRRNTIAPNCA 240
QY 241 LPVPANCLERLRCFSDPLCRSLVDFTCHHPMDILGTCATEOSRCLRAYIGLIGTAM 300
DB 241 LPVPANCLERLRCFSDPLCRSLVDFTCHHPMDILGTCATEOSRCLRAYIGLIGTAM 300
QY 301 TPNEFVSNTSVALSCTCRGSGNLQECCEMTEGFFSHNPCLTEAIAAKRRHSOLFSDQM 360
DB 301 TPNEFVSNTSVALSCTCRGSGNLQECCEMTEGFFSHNPCLTEAIAAKRRHSOLFSDQM 360
QY 361 PPHTEFAVAHONENPAVRPOPWPVPSLFCSTLPLILLISLM 400
DB 361 PPHTEFAVAHONENPAVRPOPWPVPSLFCSTLPLILLISLM 400

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RESULT 3
ID W84186
AC W84186;
DE 25-MAR-1999 (first entry)
DE Glial cell line-derived neurotrophic factor receptor gamma 2.
KW Glial cell line-derived neurotrophic factor receptor gamma 2;
KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma2;
KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
KW renal disorder; kidney failure; gut dysfunction; regeneration;
KW cardiomyocyte; epithelium; hepatocyte.
OS Homo sapiens.
FH Key
FT Location/Qualifiers
FT 1..31
FT /label= "signal-peptide
FT 32..400
FT /label= "mature protein
FT 32..382
FT /note= "extracellular domain"
FT 383..400
FT /note= "transmembrane domain"
PD M09B51056-A2.
PD 26-NOV-1998
PD 20-MAY-1998; U10328.
PR 27-JUN-1997; US-884638.
PR 20-MAY-1997; US-047092.
PR (HUMA-) HDMAN GENOME SCI INC.
PA Gentz RL, Hsu T, Ni J, Ruben SM, Young P;
WPI: 99-070150/06.
N-PSDB: V93934.
DR New isolated glial cell derived neurotrophic factor receptors - used
PT to develop products for treating e.g. neurodegenerative disorders,
PT schizophrenia, hypertension, tumours, renal disorders, kidney
PT failure or gut dysfunction
PS Claim 53; Fig 7A-D; 15pp; English.
CC The present sequence represents a glial cell line-derived neurotrophic
CC factor receptor gamma 2 (GDNFR-gamma2). GDNFR-gamma2 shares high homology
CC with GDNFR-alpha, which is capable of complexing with glial cell
CC line-derived neurotrophic factor (GDNF) and mediating cell response to
CC GDNF. The GDNFR polypeptides and agonists can be used for treating
CC polypeptides. They can be used for treating neurodegenerative diseases
CC such as amyotrophic lateral sclerosis, Parkinson's disease,
CC schizophrenia, insomnia, tardive dyskinesia, hypertension, pituitary
CC adenomas, hyperprolactinemia, thyroid tumour, renal disorders, kidney
CC failure, gut dysfunction, or for regeneration of cardiomyocytes,

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CC epithelium or hepatocytes. Antagonists of the polypeptides can be used
 CC for treating disorders associated with increased activity of the
 CC respective polypeptides. The products can also be used for detection,
 CC diagnosis and drug screening.
 SQ Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 1; Length 400;
 Best Local Similarity 100.0%; Pred. No. 5,8e-188;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYRLNRPPLPPVYLMILLPLPSPLPLAAGDPLTESRLMNSCLQARRRQADPTCSAA 60
 DB 1 MYRLNRPPLPPVYLMILLPLPSPLPLAAGDPLTESRLMNSCLQARRRQADPTCSAA 60
 QY 61 YHHDSCSTSTPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACDIYTV 120
 DB 61 YHHDSCSTSTPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACDIYTV 120
 QY 121 HRASLGNELDVSPYEDYTSKPMKNLSKLNMLKPSDCLCFAMLCITLNDKDLRK 180
 DB 121 HRASLGNELDVSPYEDYTSKPMKNLSKLNMLKPSDCLCFAMLCITLNDKDLRK 180
 QY 181 AYGACGPGHQRHVCRLQLLTFFERKAEPPHAGLLCPAPNDRGGERRRNTIAPNCA 240
 DB 181 AYGACGPGHQRHVCRLQLLTFFERKAEPPHAGLLCPAPNDRGGERRRNTIAPNCA 240
 QY 241 LPPVAPNCLERLRCFSDPLCRSLVDYFOTCHPMDLTGTCATEQSRLRAYLIGITAM 300
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDYFOTCHPMDLTGTCATEQSRLRAYLIGITAM 300
 QY 301 TPNFVSNVNTSVASCRCRSGNLQEECEMLEGFFSHNPCLTEAIAAKMRHSOLFSDW 360
 DB 301 TPNFVSNVNTSVASCRCRSGNLQEECEMLEGFFSHNPCLTEAIAAKMRHSOLFSDW 360
 QY 361 PHPTFAVMAHONENPAVRPOPWPVSLFSCITPLILLISLM 400
 DB 361 PHPTFAVMAHONENPAVRPOPWPVSLFSCITPLILLISLM 400

RESULT 4

W64180 standard; Protein; 400 AA.
 AC W64180;
 DT 25-MAR-1999 (first entry)
 DE A GDNFR-alpha-related protein 3 (GRR3).
 KW Human; glial cell-line derived neurotrophic factor receptor;
 KW GDNFR; glial cell line-derived neurotrophic factor; GDNF;
 KW neurturin; signal transduction; dopaminergic nerve cell;
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KW neurological disorder; diabetes; glaucoma; sensory neuron;
 KW retinal ganglion cell degeneration; sensory neuropathy;
 KW retinopathy; gene therapy; GDNFR-related protein 3; GRR3.
 OS Homo sapiens.
 PN W09844213-A2.
 PF 03-DEC-1998;
 PR 27-APR-1998; U08486.
 PR 30-MAY-1997; US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jling S, Wen D;
 DR WPI-98-080806/07.
 DR N-PSDB; V99329.
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 PT used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 PS or amyotrophic lateral sclerosis
 PS Claim 51; Fig 15; 318pp; English.
 CC The present sequence represents a human glial cell-line derived
 CC neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3).
 CC The protein has similar functions to GDNFR. GDNFR proteins are
 CC functionally characterised by the ability to bind glial cell
 CC line-derived neurotrophic factor (GDNF) and/or neurturin specifically,
 CC and to act as part of a molecular complex which mediates or enhances

CC the signal transduction affects of GDNF and/or neurturin. The proteins
 CC can be used for treating improperly functioning dopaminergic nerve
 CC cells, Parkinson's disease, Alzheimer's disease or amyotrophic lateral
 CC sclerosis. They can also be used for treating neurological disorders
 CC associated with diabetes, glaucoma or other diseases and conditions
 CC involving retinal ganglion cell degeneration, sensory neuropathy caused
 CC by injury to, insults to, or degeneration of, sensory neurons,
 CC pathological conditions, or disease or injury-related retinopathies.
 CC The products can also be used for detection, diagnosis, drug screening
 CC and gene therapy.
 SQ Sequence 400 AA;

Query Match 99.8%; Score 2186; DB 1; Length 400;
 Best Local Similarity 99.8%; Pred. No. 1.3e-187;
 Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYRLNRPPLPPVYLMILLPLPSPLPLAAGDPLTESRLMNSCLQARRRQADPTCSAA 60
 DB 1 MYRLNRPPLPPVYLMILLPLPSPLPLAAGDPLTESRLMNSCLQARRRQADPTCSAA 60
 QY 61 YHHDSCSTSTPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACDIYTV 120
 DB 61 YHHDSCSTSTPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACDIYTV 120
 QY 121 HRASLGNELDVSPYEDYTSKPMKNLSKLNMLKPSDCLCFAMLCITLNDKDLRK 180
 DB 121 HRASLGNELDVSPYEDYTSKPMKNLSKLNMLKPSDCLCFAMLCITLNDKDLRK 180
 QY 181 AYGACGPGHQRHVCRLQLLTFFERKAEPPHAGLLCPAPNDRGGERRRNTIAPNCA 240
 DB 181 AYGACGPGHQRHVCRLQLLTFFERKAEPPHAGLLCPAPNDRGGERRRNTIAPNCA 240
 QY 241 LPPVAPNCLERLRCFSDPLCRSLVDYFOTCHPMDLTGTCATEQSRLRAYLIGITAM 300
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDYFOTCHPMDLTGTCATEQSRLRAYLIGITAM 300
 QY 301 TPNFVSNVNTSVASCRCRSGNLQEECEMLEGFFSHNPCLTEAIAAKMRHSOLFSDW 360
 DB 301 TPNFVSNVNTSVASCRCRSGNLQEECEMLEGFFSHNPCLTEAIAAKMRHSOLFSDW 360
 QY 361 PHPTFAVMAHONENPAVRPOPWPVSLFSCITPLILLISLM 400
 DB 361 PHPTFAVMAHONENPAVRPOPWPVSLFSCITPLILLISLM 400

RESULT 5

W65117 standard; Protein; 400 AA.
 AC W65117;
 DT 28-SEP-1998 (first entry)
 DE Human GDNF alpha-3 receptor protein #2.
 KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
 KW treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve trauma;
 KW Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
 KW muscular dystrophy; diagnostic.
 OS Homo sapiens.
 PN Key
 FT Location/Qualifiers
 FT 1..400
 FT /label= GDNF alpha-3
 FT /note= "Partial sequence"
 EP-846764-A2.
 PD 10-JUN-1998.
 PD 20-NOV-1997; 309375.
 PR 09-MAY-1997; GB-009463.
 PR 27-NOV-1996; GB-024677.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 PI Lawrence GMP;
 DR WPI: 98-299980/27.
 DR N-PSDB; V35365.
 PT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
 PT used to treat neuro degenerative diseases, muscular diseases and

EM myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN W09744356-A2
 PD 27-MAY-1997; US-017426.
 PR 07-MAY-1997; US-017427.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 MPI: 98-018431/02.
 DR N-PSDB; V00250.
 DR New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 81-82; 113pp; English.
 This amino acid sequence comprises a human Ret ligand (RetL) RetL3
 partial polypeptide sequence, deduced from a partial clone (see
 V00250) isolated from a human adult heart cDNA library; a
 full-length RetL3 sequence (see W37463) is also claimed, as well
 as rat and human RetL, human RetL2 and mouse RetL3 sequences
 (see W37455-61). RetL ligand is a key component of the Ret
 signalling pathway that specifically interacts with Ret receptor
 protein, triggering Ret dimerisation and/or autophosphorylation of
 the Ret tyrosine kinase domain. Vectors containing RetL3 DNA and
 prokaryotic or eukaryotic host cells transformed or transfected
 with these vectors are claimed, as well as a method for production
 of RetL3, its soluble variants and fusion proteins with a toxin,
 imageable compound or radionuclide. RetL3, optionally when
 expressed from vectors in vivo, is used to promote growth of new
 tissue and survival of damaged tissue, particularly kidney or
 neural tissue. Typical applications are in renal failure,
 nephritis, kidney transplants, toxic or hypoxic injury,
 neurodegeneration, motor neurone disease, multiple sclerosis,
 bacterial, viral or prion infections (e.g. meningitis, myelopathy
 associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 spinal cord injury, developmental disorders such as Down's syndrome
 and cerebral palsy, or conditions involving the peripheral nervous
 system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 315 AA.
 SQ
 Query Match 78.0%; Score 1708; DB 1; Length 315;
 Best Local Similarity 100.0%; Pred. No. 5e-145;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 92 QLRNSSLICGCMCHRRKKNVACLDIYTVHARRSLGNYELDVSPYEDTVSKPKMKMLSK 151
 7 QLRNSSLICGCMCHRRKKNVACLDIYTVHARRSLGNYELDVSPYEDTVSKPKMKMLSK 66
 152 LNNLKPDSDLCTKFAMLCTLNKCDRLKRAYGACSGPHCORHVCRLQLTFFEKAAEPH 211
 67 LNNLKPDSDLCTKFAMLCTLNKCDRLKRAYGACSGPHCORHVCRLQLTFFEKAAEPH 126
 212 AGLLLCPCAPNDRCGGERRRNTIAPNCALPPVAPNCLERLRCFSDPLCRSLVDFOTR 271
 127 AGLLLCPCAPNDRCGGERRRNTIAPNCALPPVAPNCLERLRCFSDPLCRSLVDFOTR 186
 272 CHPMDILGATCATEQSRLRAYLGLTAMTPNPNVNVNTSVALSCORSGNLOECCEML 331
 187 CHPMDILGATCATEQSRLRAYLGLTAMTPNPNVNVNTSVALSCORSGNLOECCEML 246
 332 EEFESHNPCLTAIAAKMFFHSOLFSDQMPHPTFAVAHONENPAVPOPWVPSLSCSL 391
 247 EEFESHNPCLTAIAAKMFFHSOLFSDQMPHPTFAVAHONENPAVPOPWVPSLSCSL 306
 392 PLILLSLW 400
 307 PLILLSLW 315

RESULT 8
 W37461
 ID W37461 standard; Protein; 397 AA.
 AC W37461;
 DT 21-MAY-1998 (first entry)
 DE Mouse Ret ligand RetL3.
 KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Mus musculus.
 PN W09744356-A2.
 PD 27-NOV-1997.
 PR 07-MAY-1997; US-017426.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 MPI: 98-018431/02.
 DR N-PSDB; V00249.
 DR New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 77-78; 113pp; English.
 This amino acid sequence comprises mouse Ret ligand (RetL) RetL3,
 CC deduced from cDNA clones (see V00249) isolated from an EST
 CC database and by 5'RACE. Rat and human RetL, human RetL2 and RetL3
 CC sequences (see W37457-60 and W37462-63) are also claimed. RetL is
 CC a key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing RetL3 DNA and prokaryotic or eukaryotic host
 CC cells transformed or transfected with these vectors are claimed, as
 CC well as a method for production of RetL3. Its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL3, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 397 AA.
 SQ
 Query Match 75.2%; Score 1646.5; DB 1; Length 397;
 Best Local Similarity 77.8%; Pred. No. 2.1e-139;
 Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;
 9 PLPPVTLMLLLIPSPPLDLAGDPLPTESRLMNSCLQARRCOADPTCSAAVHHLDSCT 68
 7 PRPP-LIMILLIVLSMLPLGAGNSLATENRFVNSCTQARKKCEANPAKAAVYHLSGCT 65
 69 SSTSTLPSSEBSPVADCEAAQOLRNSSLICGCMCHRRKKNVACLDIYTVHARRSLGN 128
 66 SSTSRPLPLEESMSADCEAAEQOLRNSSLIDCRCHRRKHQATCDIYTVHARRSLGD 125
 129 YELDVSPYEDTVSKPKMKMLSKLNNLKPDSDLCTKFAMLCTLNKCDRLKRAYGACSG 188

DB 126 YELDVSPYEDVTYVSKPKMNLSTLMKLPDSDCLCFAMCTLDKCDRLKAYGECG 185
 QY 189 PRCORHVCLOLLTFEKAEPHAGILLPCAPNDRCGERRNTIAPCALPVPAPNC 248
 DB 186 IRCORHVCLOLLTFEKAEPHAGILLPCAPNDRCGERRNTIAPCALPVPAPNC 245
 QY 249 LEIRLRCFSPPLCRSLVDTQTHCHPMIDIGTCATDSCRLRAYLGLIGTAMPNPNV 308
 DB 246 LDLSFCRADPLCRSLVDTQTHCHPMIDIGTCATDSCRLRAYLGLIGTAMPNPNV 305
 QY 309 NTVALSCTRGSGNLQDECEMLEGFFSHNPCLTEATAAMRRHSOLFSDQWHPPTAV 368
 DB 306 NTVALSCTRGSGNLQDECEMLEGFFSHNPCLTEATAAMRRHSOLFSDQWHPPTAV 365
 QY 369 AHONENPVRPQWPVPSLFCSTPLILLISLW 400
 DB 366 QOONSNPALRLOPLRPLFSILPLILLQTLW 397

RESULT 9
 182
 W84182 standard; Protein: 397 AA.

AC W84182;
 DT 25-MAR-1999 (first entry)
 DE A GDNFR-alpha-related protein 3 (GRR3).
 KW Rat; glial cell-line derived neurotrophic factor receptor;
 KW GDNFR; glial cell-line derived neurotrophic factor; GDNF;
 KW neurturin; signal transduction; dopaminergic nerve cell;
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KW neurological disorder; diabetes; glaucoma; sensory neuron;
 KW retinal ganglion cell degeneration; sensory neuronopathy;
 KW retinopathy; gene therapy; GDNFR-related protein 3; GRR3.
 OS Rattus sp.
 PN WO9854213-A2.
 PD 03-DEC-1998.
 PE 27-APR-1998: U08486.
 PR 30-MAY-1997: US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR N-PSDB: V99331.
 DR N-PSDB: 99-080806/07.

PT New isolated glial cell line-derived neurotrophic factor receptors -
 PT used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 PT or amyotrophic lateral sclerosis.
 PS Clam 51; Fig 17; 318pp; English.

CC The present sequence represents a rat glial cell-line derived
 CC neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3).
 CC The protein has similar functions to GDNFR. GDNFR proteins are
 CC functionally characterized by the ability to bind glial cell
 CC line-derived neurotrophic factor (GDNF) and/or neurturin specifically,
 CC and to act as part of a molecular complex which mediates or enhances
 CC the signal transduction affects of GDNF and/or neurturin. The proteins
 CC can be used for treating improperly functioning dopaminergic nerve
 CC cells, Parkinson's disease, Alzheimer's disease or amyotrophic lateral
 CC sclerosis. They can also be used for treating neurological disorders
 CC associated with diabetes, glaucoma or other diseases and conditions
 CC involving retinal ganglion cell degeneration, sensory neuropathy caused
 CC by injury to, insults to, or degeneration of, sensory neurons,
 CC pathological conditions, or disease or injury-related retinopathies.
 CC The products can also be used for detection, diagnosis, drug screening
 CC and gene therapy.
 SQ Sequence 397 AA;

Query Match 75.0%; Score 1642.5; DB 1; Length 397;
 Best Local Similarity 77.2%; Pred. No. 4.8e-139;
 Matches 305; Conservative 30; Mismatches 57; Indels 3; Gaps 1;

QY 6 NRPRLPVVLMILLPPSPPLAGDPLPESRLMNSCLARRKQADPTCSAAYHLD 65
 DB 6 SPRPPLVILLVLST--WLPDGTGNSLPFTENRNVNCTQARKKCEANPACKAAYCHD 62

QY 66 SCTSSISTPLPSEEPVADCLAAOOLRNSLIGCCRRMKNOVACLDIYTVHARS 125
 DB 63 SCPPSLSPPLPSEESATSAACLEAAOOLRNSLIDCRHRMKHOATCDIYTVHARS 122
 QY 126 LSNVELDVSPYEDVTYVSKPKMNLSTLMKLPDSDCLCFAMCTLDKCDRLKAYG 185
 DB 123 LSNVELDVSPYEDVTYVSKPKMNLSTLMKLPDSDCLCFAMCTLDKCDRLKAYG 182
 QY 186 CSPPHOCORHVCLOLLTFEKAEPHAGILLPCAPNDRCGERRNTIAPCALPVP 245
 DB 183 CSPPHOCORHVCLOLLTFEKAEPHAGILLPCAPNDRCGERRNTIAPCALPVP 242
 QY 246 PNCLEFRRCFSDPLCRSLVDTQTHCHPMIDIGTCATDSCRLRAYLGLIGTAMPN 305
 DB 243 PNCLEFRRCFSDPLCRSLVDTQTHCHPMIDIGTCATDSCRLRAYLGLIGTAMPN 302
 QY 306 SNVTVALSCTRGSGNLQDECEMLEGFFSHNPCLTEATAAMRRHSOLFSDQWHP 365
 DB 303 SNVTVALSCTRGSGNLQDECEMLEGFFSHNPCLTEATAAMRRHSOLFSDQWHP 362
 QY 366 AYMAHONENPVRPQWPVPSLFCSTPLILLISLW 400
 DB 363 SYVQOONSNPALRLOPLRPLFSILPLILLQTLW 397

RESULT 10
 W37465
 AC W37465;
 DT 21-MAY-1998 (first entry)
 DE Mouse Ret ligand retL3 partial sequence.
 KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neuron disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Mus musculus.
 PN WO9744356-A2.
 PD 27-NOV-1997.
 PE 07-MAY-1997: U07726.
 PR 10-APR-1997: US-017427.
 PR 08-MAY-1996: US-017427.
 PR 07-JUN-1996: US-019300.
 PR 16-JUL-1996: US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR WPI: 98-018431/02.
 DR N-PSDB: V00256.

PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Disclosure: Page 73-74; 113pp; English.
 CC This polypeptide comprises a partial sequence of mouse Ret ligand
 CC RetL3, deduced from EST A4050083 cDNA (see V00256). A full-length
 CC mouse RetL3 sequence (see W37461) was also obtained. Rat, mouse
 CC and human RetL1, RetL2 and RetL3 cDNA sequences (see V00245-51) and
 CC encoded polypeptides (see W37457-63) are claimed and can be used
 CC in methods for promoting cell growth and improving survival of
 CC cells, especially renal or neural cells.
 SQ Sequence 346 AA;

Query Match 66.4%; Score 1455; DB 1; Length 346;
 Best Local Similarity 80.9%; Pred. No. 2.3e-122;
 Matches 267; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 71 ISPLPSEESVPADCLAAOOLRNSLIGCCRRMKNOVACLDIYTVHARSAGYE 130
 DB 17 LSRLPLEESMSADCLAAEQOLNSSLIDCRHRMKHOATCDIYTVHARSAGYE 76

QY 131 LDVSPYEDVTWTSKFWKMLSKLNLKPKSDICLAFMLCTLNDKCDRLKAYGACSGPH 190
 DB 77 LDVSPYEDVTWTSKFWKMLSKLNLKPKSDICLAFMLCTLNDKCDRLKAYGACSGPH 136
 QY 191 CORAVCLRLTFFERKAEPHAGLILCPAPNDRCGERRRNTIAPCALPPVAPNLE 250
 DB 137 CORHLCALQLEFFERKAESHAGLILCPAPNDRCGERRRNTIAPCALPPVAPNLE 196
 QY 251 LRLCFSDPLCRSLVDFQTCHEPMDILGTATGTEOSRCLRAVLIGTIGTAMPNPNVSNNT 310
 DB 197 LRSCGRADPLCRSLVDFQTCHEPMDILGTATGTEOSRCLRAVLIGTIGTAMPNPNVSNNT 256
 QY 311 SVALSCTCRSGNLOECCEMLEGFFSHNPCLTEAIAAMRPHSOLFSDMPHPTFAVAH 370
 DB 257 TVALSCTCRSGNLOECCEMLEGFFSHNPCLTEAIAAMRPHSOLFSDMPHPTFAVAH 316
 QY 371 QNENPVRPQWVPSLSCITPLILSLW 400
 DB 317 QNSNPALRLQPRPLILSILPLILQTLW 346

RESULT 11

W65118
 ID W65118 standard; Protein; 172 AA.
 AC W65118;
 DE 28-SEP-1998 (first entry)
 KW Human GDNF alpha-3 receptor protein fragment.
 KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
 KW treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
 KW Huntington's disease; Alzheimer's disease; diabetic neuropathy; muscle;
 KW muscular dystrophy; diagnostic.
 OS Homo sapiens.
 FH Key
 FT Location/Qualifiers
 FT 1..172
 FT /label= "GDNF alpha-3
 FT /note= "Partial sequence"
 EP-846764-A2.
 PN 10-JUN-1998.
 PF 20-NOV-1997; 309375.
 PR 09-MAY-1997; GB-009463.
 PR 27-NOV-1996; GB-024677.
 PA (SMIR) SMITHKLINE BEECHAM PLC.
 PI Lawrence GMP;
 DR WPI: 98-299980/27.
 N-PSDB: V35366.
 CC New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
 used to treat neuro degenerative diseases, muscular diseases and
 nerve and muscle trauma and in diagnostic assays
 PT Claim 29; Fig 6; 22pp; English.
 CC This sequence represents a fragment from a novel glial cell line-derived
 neurotrophic factor alpha-3 receptor (GDNF alpha-3). This protein can be
 used to treat e.g. neurodegenerative diseases (such as Parkinson's
 Disease), amyotrophic lateral sclerosis (ALS), spinal muscular atrophy
 (SMA), Huntington's Disease, Alzheimer's Disease, diabetic neuropathy,
 CC muscular diseases (including the muscular dystrophies) and nerve and
 CC muscle trauma and in diagnostic assays for such conditions.
 SQ Sequence 172 AA.

Query Match 43.1%; Score 944; DB 1; Length 172;
 Best Local Similarity 100.0%; Pred. No. 4.3e-77;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ERRRNTIAPCALPPVAPNLELRLCFSDPLCRSLVDFQTCHEPMDILGTATGTEOSRC 288
 DB 1 ERRRNTIAPCALPPVAPNLELRLCFSDPLCRSLVDFQTCHEPMDILGTATGTEOSRC 60
 QY 289 LRAVLIGTIGTAMPNPNVSNNTSVALSCTCRSGNLOECCEMLEGFFSHNPCLTEAIAAR 348
 DB 61 LRAVLIGTIGTAMPNPNVSNNTSVALSCTCRSGNLOECCEMLEGFFSHNPCLTEAIAAR 120

QY 349 MRHSQLESDMPHPTFAVAHONENPAVRPQWVPSLSCITPLILSLW 400
 DB 121 MRHSQLESDMPHPTFAVAHONENPAVRPQWVPSLSCITPLILSLW 172

RESULT 12

W84183
 ID W84183 standard; Protein; 498 AA.
 AC W84183;
 DE 25-MAR-1999 (first entry)
 KW Consensus sequence of rat and human GDNF and GRN proteins.
 KW Glial cell-line derived neurotrophic factor receptor;
 KW GDNF; glial cell line-derived neurotrophic factor; GDNF;
 KW neurotrophin; signal transduction; dopaminergic nerve cell;
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KW neurological disorder; diabetes; glaucoma; sensory neuron;
 KW retinal ganglion cell degeneration; sensory neuropathy;
 KW retinopathy; gene therapy; GDNF-related protein; GRN.
 OS Synthetic.
 OS Rattus sp.
 OS Homo sapiens.
 FH Key
 FT Location/Qualifiers
 FT MISC.difference 1..498
 FT /note= "x-not specified"
 PN W09854213-A2.
 PD 03-DEC-1998.
 PF 27-APR-1998; U08486.
 PR 30-MAY-1997; US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR WPI: 99-080806/07
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 PT or amyotrophic lateral sclerosis
 PS Claim 51; Fig 19; 31pp; English.
 CC The present sequence represents a consensus sequence of rat and
 CC human glial cell-line derived neurotrophic factor receptor (GDNF)
 CC protein and GDNF-related (GRN) proteins. The proteins have similar
 CC functions. GDNF proteins are functionally characterized by the ability
 CC to bind glial cell line-derived neurotrophic factor (GDNF) and/or
 CC neurotrophin specifically, and to act as part of a molecular complex which
 CC mediates or enhances the signal transduction affects of GDNF and/or
 CC neurotrophin. The proteins can be used for treating improperly functioning
 CC dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease or
 CC amyotrophic lateral sclerosis. They can also be used for treating
 CC neurological disorders associated with diabetes, glaucoma or other
 CC diseases and conditions involving retinal ganglion cell degeneration,
 CC sensory neuropathy caused by injury to, insults to, or degeneration of,
 CC sensory neurons, pathological conditions, or disease or injury-related
 CC retinopathies. The products can also be used for detection, diagnosis,
 CC drug screening and gene therapy.
 SQ Sequence 498 AA;

Query Match 28.9%; Score 632.5; DB 1; Length 498;
 Best Local Similarity 40.2%; Pred. No. 1.2e-48;
 Matches 151; Conservative 24; Mismatches 166; Indels 35; Gaps 10;

QY 1 MVRPLNRPPLPYVLMILLPLPSPLPLA---GDPPLPESRLMNSCLQARRKCOADPTC 57
 DB 1 MVRPLNRPPLPYVLMILLPLPSPLPLA---GDPPLPESRLMNSCLQARRKCOADPTC 59
 QY 58 SAAVNHLDSCS--SISTPLPS-EEPSVPADCLAAQOLRNSSLICMCHRRKKNQVACT 114
 DB 60 SXXYRRLRQCGXGXNNTLASGXEXXKXKXAXEXLXSLVYCRCKRKKKEXXCL 119
 QY 115 DIYWTYHRAHSLGNLYLADVSPYEDVTWTSKFWKMLSKL-----NMLKPSDOL 161
 DB 120 XIYWSXHXKXKXGXNNTLASGXEXXKXKXAXEXLXSLVYCRCKRKKKEXXCL 174
 QY 162 CLKFALCTLNDKCDRLKAYGAC-----SGPHOGRHVCNLQTLFFERKAEPHAGSL 216

Db 175 CLDAARCNLDNDCKIKRSYIYXCCXXXSKRCNRRCKALROFEDVPYXXHYGML 234
 QY 217 LCPADPNDRCCGERRRTIAPNCALPPV-APNCLLELRCLFSDPLCRSLVDQTHC--H 273
 Db 235 FCGCXXXDXACXERRRRTIPSCSYEXXKPNCLDLRXKRTIXLRSRLADYXICXXX 294
 QY 274 PNDILGTCATGSRCLRAYIGLIGTAMTFVSNVT--SVALSCTCRSGNLQEECEML 331
 Db 295 XRXVXSCXAXNYXXCLXAYGLIGTMTPTVDSXKXXVAPWCXCRSGNXXECCNF 354
 QY 332 EGFESHNPCLTEAIAA 347
 Db 355 LAFEXXNPCLXNAIOA 370

RESULT 13

W84298
 ID W84298
 AC W84298; standard; Protein: 489 AA.
 PM 25-MAR-1999 (first entry)

Consensus sequence of GDNFR and GRR2 and GRR3 proteins.
 Glial cell-line derived neurotrophic factor receptor;
 GDNFR; glial cell line-derived neurotrophic factor; GDNF;
 neurturin; signal transduction; dopaminergic nerve cell;
 Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 neurological disorder; diabetes; glaucoma; sensory neuron;
 retinal ganglion cell degeneration; sensory neuropathy;
 retinopathy; gene therapy; GDNFR-related protein; GRR2; GRR3.
 OS Synthetic.
 KW retinopathy; gene therapy; GDNFR-related protein; GRR2; GRR3.
 KM retinopathy; gene therapy; GDNFR-related protein; GRR2; GRR3.
 KS retinopathy; gene therapy; GDNFR-related protein; GRR2; GRR3.
 OS Synthetic.

Key Location/Qualifiers
 Misc-difference 1..489
 /note="x-not specified"

PD W09854213-A2.
 PE 03-DEC-1998.
 PF 27-APR-1998; U08486.
 PR 30-MAY-1997; US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR WPI: 99-080806/07.
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 used to develop products for treating e.g. improperly functioning
 dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 or amyotrophic lateral sclerosis.
 PS Claim 51; Fig 26; 318pp; English.
 CC The present sequence represents a consensus sequence of glial
 cell-line derived neurotrophic factor receptor (GDNFR) protein and
 GDNFR-related (GRR) proteins GRR2 and GRR3. The proteins have similar
 functions. GDNFR proteins are functionally characterized by the ability
 to bind glial cell line-derived neurotrophic factor (GDNF) and/or
 neurturin specifically, and to act as part of a molecular complex which
 mediates or enhances the signal transduction affects of GDNF and/or
 neurturin. The proteins can be used for treating improperly functioning
 dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease or
 amyotrophic lateral sclerosis. They can also be used for treating
 neurological disorders associated with diabetes, glaucoma or other
 diseases and conditions involving retinal ganglion cell degeneration,
 sensory neuropathy caused by injury to, insults to, or degeneration of,
 sensory neurons, pathological conditions, or disease or injury-related
 retinopathies. The products can also be used for detection, diagnosis,
 drug screening and gene therapy.
 SQ Sequence 489 AA.

Query Match 26.9%; Score 589.5; DB 1; Length 489;
 Best Local Similarity 38.8%; Pred. No. 8e-45;
 Matches 134; Conservative 22; Mismatches 160; Indels 29; Gaps 8;

QY 27 PLAADPPTESRLMNSCLQARRCOADPTCSAAVHHLDSCT-SISYPLPSEPSVPAD 85
 Db 24 PLXIXXKX 83
 QY 86 CLEAAGQRLNSLIGCMCHRRMKNOVACLDITWYHARRSLGNTLEDVSPEDTIVTSKFW 145

Db 84 CXXAXEXIXXSSLYDRCRGKREXCLXIYWSHXXLXKXKXKXLESPYPTSR-- 142
 QY 146 KMLSKL-----NKLKPSDLCLEFAMLCITLNDGDLRRAYGAC-----S 187
 Db 142 ---LSDIFRXKX 198
 QY 188 GPHCORHVCRLRLTFEFAEAPHAQGLILCPCANDRDCCGERRRTIAPNCALPPV-AP 246
 Db 199 XRCRRRCRCKRLROFFEDVPYXXHYGMLFCGXXXDXACXERRRQTIKPCSYEXXEXP 258
 QY 247 NCLLELRCLFSDPLCRSLVDQTHCHPMDILGT-C-ATEGSRCLRAYIGLIGTAMTFV 304
 Db 259 NCLDLRSKCRDPLCRSLADPXTKCPXKX 318
 QY 305 VSNVNT--SVALSCTCRSGNLQEECEMLGEFFSHNPCLTEAIAA 347
 Db 319 VDSKXKXKXVAPWCXCRSGNXXECCERFLXKX 363

RESULT 14

W84181
 ID W84181
 AC W84181; standard; Protein: 460 AA.
 PM 25-MAR-1999 (first entry)

DE A GDNFR-alpha-related protein 2 (GRR2).
 KW Rat; glial cell-line derived neurotrophic factor receptor;
 GDNFR; glial cell line-derived neurotrophic factor; GDNF;
 neurturin; signal transduction; dopaminergic nerve cell;
 Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 neurological disorder; diabetes; glaucoma; sensory neuron;
 retinal ganglion cell degeneration; sensory neuropathy;
 retinopathy; gene therapy; GDNFR-related protein 2; GRR2.
 KM retinopathy; gene therapy; GDNFR-related protein 2; GRR2.
 KW retinopathy; gene therapy; GDNFR-related protein 2; GRR2.
 KS retinopathy; gene therapy; GDNFR-related protein 2; GRR2.

OS Rattus sp.
 PD W09854213-A2.
 PE 03-DEC-1998.
 PF 27-APR-1998; U08486.
 PR 30-MAY-1997; US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR WPI: 99-080806/07.
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 used to develop products for treating e.g. improperly functioning
 dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 or amyotrophic lateral sclerosis.
 PS Claim 51; Fig 16; 318pp; English.
 CC The present sequence represents a rat glial cell-line derived
 neurotrophic factor receptor (GDNFR)-related protein 2 (GRR2).
 CC The protein has similar functions to GDNFR. GDNFR proteins are
 functionally characterized by the ability to bind glial cell
 line-derived neurotrophic factor (GDNF) and/or neurturin specifically,
 and to act as part of a molecular complex which mediates or enhances
 the signal transduction affects of GDNF and/or neurturin. However,
 neurturin binds GRR2 more effectively than GDNF, while the reverse is
 true for GDNFR. The proteins can be used for treating improperly
 functioning dopaminergic nerve cells, Parkinson's disease, Alzheimer's
 disease or amyotrophic lateral sclerosis. They can also be used for
 treating neurological disorders associated with diabetes, glaucoma or
 other diseases and conditions involving retinal ganglion cell
 degeneration, sensory neuropathy caused by injury to, insults to, or
 degeneration of, sensory neurons, pathological conditions, or disease or
 injury-related retinopathies. The products can also be used for
 detection, diagnosis, drug screening and gene therapy.
 SQ Sequence 460 AA.

Query Match 25.0%; Score 547.5; DB 1; Length 460;
 Best Local Similarity 36.0%; Pred. NO. 4.2e-41;
 Matches 131; Conservative 45; Mismatches 139; Indels 49; Gaps 11;

QY 19 LLPLPSPPLAADPPTESRLMNS-----CLQARRCOADPTCSAAVHHLDSCT 68
 Db 1 MLVPSHYPETIRSLASPSLGSSELHGMRPQYDCVRAHELCAABSCSSRTITLNOCL 60

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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:27:09 ; Search time 29.27 Seconds

(without alignments)
298,605 Million cell updates/sec

Title: US-09-272-835-17

Perfect score: 2022

Sequence: 1 MVRPLNRPPLPPVYVIMLLLPSPPLPSFCTPLILILSLIM 369

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

abase: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1996.5	98.7	400	1	W37463	Human Ret ligand R
2	1996.5	98.7	400	1	W65116	Human GDNF alpha-3
3	1996.5	98.7	400	1	W84186	Gli1 cell line-de
4	1992.5	98.5	400	1	W84180	A GDNFR-alpha-rela
5	1990.5	98.4	400	1	W65117	Human GDNF alpha-3
6	1849.5	91.5	378	1	W84185	Gli1 cell line-de
7	1514.5	74.9	315	1	W37462	Human Ret ligand R
8	1459	72.2	397	1	W84182	A GDNFR-alpha-rela
9	1458	72.1	397	1	W37461	Mouse Ret ligand R
10	1266.5	62.6	372	1	W37465	Mouse Ret ligand R
11	944	46.7	142	1	W65118	Human GDNF alpha-3
12	579	28.6	498	1	W84183	Consensus sequence
13	544	26.9	489	1	W84298	A GDNFR-alpha-rela
14	519	25.7	460	1	W84181	Rat neurotulin rece
15	514	25.4	464	1	W1604	Rat neurotulin rece
16	514	25.4	464	1	W1602	Consensus sequence
17	513	25.4	464	1	W37459	A GDNFR-alpha-rela
18	513	25.4	464	1	W81624	Rat neurotulin rece
19	513	25.4	411	1	W81625	Mouse TGF-beta pol
20	509	25.2	464	1	W37460	Human Ret ligand R
21	509	25.2	464	1	W1601	Human neurotulin re
22	509	25.2	664	1	W1603	Human neurotulin re
23	509	25.2	664	1	W81622	Human TGF-beta rel
24	509	25.2	411	1	W81623	Human mature TGF-b
25	509	25.2	464	1	W84184	Gli1 cell line-de
26	509	25.2	464	1	W84179	A GDNFR-alpha-rela
27	509	25.2	464	1	W37459	Human GDNFR-beta P
28	488	24.1	460	1	W37459	Human Ret ligand R
29	485.5	24.0	465	1	W35333	Human Ret ligand R
30	485.5	24.0	465	1	W84163	Gli1 cell line-de
31	485.5	24.0	463	1	W84166	GDNFR-alpha protei
32	485.5	24.0	463	1	W84167	GDNFR-alpha protei
33	485.5	24.0	465	1	W92300	Human GDNFR-alpha
34	484.5	24.0	465	1	W84165	GDNFR-alpha protei
35	483.5	23.9	468	1	W27327	Rat gli1 cell der
36	483.5	23.9	468	1	W35334	Rat gli1 cell lin
37	483.5	23.9	468	1	W37457	Rat Ret ligand Rel
38	483.5	23.9	468	1	W84164	Gli1 cell-line de
39	476.5	23.6	468	1	W84164	Gli1 cell-line de
40	407	20.1	360	1	W22298	Rat GDNFR-alpha po
41	403	19.9	331	1	W81627	Mouse TGF-beta rel
42	379.5	18.8	346	1	W37458	Human Ret ligand R
43	336.5	16.6	232	1	W84168	GDNFR-alpha protei

ALIGNMENTS

RESULT	1
W37463	
ID	W37463 standard; Protein; 400 AA.
AC	W37463.
DT	21-MAY-1998 (first entry)
DE	Human Ret ligand, RetL3.
KW	Ret ligand; RetL3; receptor; signal transduction; human;
KW	cell growth; renal cell; nerve cell; renal failure; nephritis;
KW	kidney transplant; toxic injury; hypoxic injury;
KW	neurodegeneration; motor neurone disease; multiple sclerosis;
KW	infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW	cerebral palsy; Lyme disease; muscular dystrophy;
KW	myasthenia gravis; tumour; therapy.
OS	Homo sapiens.
PN	W09744356.A2.
PD	21-NOV-1997.
PF	07-MAY-1997; 007726.
PR	10-APR-1997; US-017427.
PR	08-MAY-1996; US-017427.
PR	07-JUN-1996; US-019300.
PR	16-JUL-1996; US-021859.
PA	(BIO) BIOGEN INC.
PI	Care M; Hesslon J.
DR	WPI; 98-018431702.
DR	N-PSDB; 000251.
PT	New nucleic acid encoding ret receptor ligands and related proteins
PT	- vectors, transformed cells and antibodies, used for promoting cell
PT	growth and improving survival of injured cells, especially renal or
PT	nerve cells
PT	Claim 2; Page 85-86; 113pp; English.
CC	This amino acid sequence comprises human Ret ligand (RetL3, RetL3,
CC	deduced from cDNA clones (see W00251) isolated from a adult heart
CC	and spinal cord libraries. Rat and human RetL1, human RetL2 and
CC	mouse RetL3 sequences (see W37457-62) are also claimed. Human
CC	RetL3 is 34.3% identical to human RetL1, 34.9% identical to human
CC	RetL2 and 76.8% identical to murine RetL3. Ret ligand is a key
CC	component of the Ret signalling pathway that specifically
CC	interacts with Ret receptor protein, triggering Ret dimerisation
CC	and/or autophosphorylation of the Ret tyrosine kinase domain.
CC	Vectors containing RetL3 DNA and prokaryotic or eukaryotic host
CC	cells transformed or transfected with these vectors are claimed, as
CC	well as a method for production of RetL3, its soluble variants and
CC	fusion proteins with a toxin, imageable compound or radionuclide.
CC	RetL3, optionally when expressed from vectors in vivo, is used to
CC	promote growth of new tissue and survival of damaged tissue, particularly
CC	kidney or neural tissue. Typical applications are in
CC	renal failure, nephritis. Kidney transplants, toxic or hypoxic
CC	injury, neurodegeneration, motor neurone disease, multiple sclerosis,
CC	bacterial, viral or prion infections (e.g. meningitis, myelopathy
CC	associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
CC	spinal cord injury, developmental disorders such as Down's syndrome
CC	and cerebral palsy, or conditions involving the peripheral nervous
CC	system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC	Fusion proteins are used to deliver toxins etc. to Ret-expressing
CC	cells, especially tumours.
CC	Sequence 400 AA;
CC	90

Query Match: 98.7% Score 1996.5; DB 1; Length 400;
Best Local Similarity: 92.2%; Pred. No. 6.9e-165;
Matches 369; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
1 MVRPLNRPPLPPVYVIMLLLPSPPLPSFCTPLILILSLIM 369
1 MVRPLNRPPLPPVYVIMLLLPSPPLPSFCTPLILILSLIM 369

QY 61 YHLDSCSSISITPLPSEPSVVPADCLAEAAQOLRNSSLIGCMCHRRMKNOVACDIYTV 120
 DB 61 YHLDSCSSISITPLPSEPSVVPADCLAEAAQOLRNSSLIGCMCHRRMKNOVACDIYTV 120
 QY 121 HRA8L-----DSDCLKFAMLCTINDKCDRLRK 149
 DB 121 HRA8L-----DSDCLKFAMLCTINDKCDRLRK 180
 QY 150 AYGCACGPHQCRHVCLROLITFEKAAEPHAGLLCPCAPNDGCGERRRNTIAPNCA 209
 DB 151 AYGCACGPHQCRHVCLROLITFEKAAEPHAGLLCPCAPNDGCGERRRNTIAPNCA 240
 QY 210 LPFVAPNCLERLRCFSDPLCRSLVDVOTCHPMDLIGTCATQOSRCLRAYLIGITAM 269
 DB 241 LPFVAPNCLERLRCFSDPLCRSLVDVOTCHPMDLIGTCATQOSRCLRAYLIGITAM 300
 QY 270 TPNFVSNVNTSVALSCTCRSGNLOEDECMELEGFFSHNPCLTEAIAAKMRHSOLFSDW 329
 DB 301 TPNFVSNVNTSVALSCTCRSGNLOEDECMELEGFFSHNPCLTEAIAAKMRHSOLFSDW 360
 QY 330 PPTFAVAHONENPAVRPOWPVSLFSCITPLILLSLW 369
 DB 361 PPTFAVAHONENPAVRPOWPVSLFSCITPLILLSLW 400

RESULT 2
 W65116
 ID W65116 standard; Protein; 400 AA.
 AC W65116; (first entry)
 DT 28-SEP-1998
 DE Human GDNF alpha-3 receptor protein #1.
 KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
 KW treatment; neurodegenerative disease; Parkinson's Disease; ALS; SMA;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
 KW Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
 KW muscular dystrophy; diagnostic.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Protein 1..400
 FT /label= GDNF alpha-3
 FT /note= "Partial sequence"
 PN EP-846764-A2.
 PD 10-JUN-1998.
 PF 20-NOV-1997; 309375.
 PR 09-MAY-1997; GB-009463.
 PR 27-NOV-1996; GB-024677.
 PA (SMIRK) SMITHKLINE BEECHAM PLC.
 LA Lawrence GMP.
 WP1: 98-299980/27.
 DK N-PSDB: V35364.
 PT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
 PT used to treat neuro degenerative diseases, muscular diseases and
 PT nerve and muscle trauma and in diagnostic assays
 PS Claim 4; Fig 2; 22pp; English.
 CC This sequence represents a novel glial cell line-derived neurotrophic
 CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to
 CC treat e.g. neurodegenerative diseases (such as Parkinson's Disease,
 CC amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA),
 CC Huntington's Disease, Alzheimer's Disease, diabetic neuropathy),
 CC muscular diseases (including the muscular dystrophies) and nerve and
 CC muscle trauma and in diagnostic assays for such conditions.
 SQ Sequence 400 AA;

Query Match 98.7% Score 1996.5; DB 1: Length 400;
 Best Local Similarity 92.2%; Pred. No. 6,9e-165;
 Matches 369; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 1 MYRLNRPRLPPLPVYIMLLLPSPPLPLAGDPLPTSRMLNSCLARRKCOADPTCSAA 60
 DB 1 MYRLNRPRLPPLPVYIMLLLPSPPLPLAGDPLPTSRMLNSCLARRKCOADPTCSAA 60

QY 61 YHLDSCSSISITPLPSEPSVVPADCLAEAAQOLRNSSLIGCMCHRRMKNOVACDIYTV 120
 DB 61 YHLDSCSSISITPLPSEPSVVPADCLAEAAQOLRNSSLIGCMCHRRMKNOVACDIYTV 120
 QY 121 HRA8L-----DSDCLKFAMLCTINDKCDRLRK 149
 DB 121 HRA8L-----DSDCLKFAMLCTINDKCDRLRK 180
 QY 150 AYGCACGPHQCRHVCLROLITFEKAAEPHAGLLCPCAPNDGCGERRRNTIAPNCA 209
 DB 181 AYGCACGPHQCRHVCLROLITFEKAAEPHAGLLCPCAPNDGCGERRRNTIAPNCA 240
 QY 210 LPFVAPNCLERLRCFSDPLCRSLVDVOTCHPMDLIGTCATQOSRCLRAYLIGITAM 269
 DB 241 LPFVAPNCLERLRCFSDPLCRSLVDVOTCHPMDLIGTCATQOSRCLRAYLIGITAM 300
 QY 270 TPNFVSNVNTSVALSCTCRSGNLOEDECMELEGFFSHNPCLTEAIAAKMRHSOLFSDW 329
 DB 301 TPNFVSNVNTSVALSCTCRSGNLOEDECMELEGFFSHNPCLTEAIAAKMRHSOLFSDW 360
 QY 330 PPTFAVAHONENPAVRPOWPVSLFSCITPLILLSLW 369
 DB 361 PPTFAVAHONENPAVRPOWPVSLFSCITPLILLSLW 400

RESULT 3
 W84186
 ID W84186 standard; Protein; 400 AA.
 AC W84186;
 DT 25-MAR-1999 (first entry)
 DE Glial cell line-derived neurotrophic factor receptor gamma 2.
 KW Glial cell line-derived neurotrophic factor receptor gamma 2;
 KW GDNF; alpha; glial cell line-derived neurotrophic factor; GDNF;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNF-gamma2;
 KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
 KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumor;
 KW renal disorder; kidney failure; gut dysfunction; regeneration;
 KW cardiomyocyte; epithelium; hepatocyte.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..31
 FT /label= signal_peptide
 FT Protein 32..400
 FT /label= mature_protein
 FT Domain 32..382
 FT /note= "extracellular domain"
 FT Domain 383..400
 FT /note= "transmembrane domain"
 PN NC09853069-A2.
 PD 26-NOV-1998.
 PF 20-MAY-1998; U10328.
 PR 27-JUN-1997; US-884638.
 PR 20-MAY-1997; US-047092.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Gentz RL, Hsu T, Ni J, Ruben SM, Young P;
 WP1: 99-070150/06.
 DK N-PSDB: V99334.
 PT New isolated glial cell derived neurotrophic factor receptors - used
 PT to develop products for treating e.g. neurodegenerative disorders,
 PT schizophrenia, hypertension, tumours, renal disorders, kidney
 PT failure or gut dysfunction
 PS Claim 53; Fig 7A-D; 156pp; English.
 CC The present sequence represents a glial cell line-derived neurotrophic
 CC factor receptor gamma 2 (GDNF-gamma2). GDNF-gamma2 shares high homology
 CC with GDNF-gamma1, which is capable of complexing with glial cell
 CC line-derived neurotrophic factor (GDNF) and mediating cell response to
 CC GDNF. The GDNF polypeptides and agonists can be used for treating
 CC disorders associated with decreased activity of the respective
 CC polypeptides. They can be used for treating neurodegenerative diseases
 CC such as amyotrophic lateral sclerosis, Parkinson's disease,
 CC schizophrenia, insomnia, tardive dyskinesia, hypertension, pituitary
 CC adenomas, hyperprolactinemia, thyroid tumour, renal disorders, kidney
 CC failure, gut dysfunction, or for regeneration of cardiomyocytes.

epithelium or hepatocytes. Antagonists of the polypeptides can be used for treating disorders associated with increased activity of the respective polypeptides. The products can also be used for detection, diagnosis and drug screening.

Query Match 98.7%; Score 1996.5; DB 1; Length 400;
Best Local Similarity 92.2%; Pred. No. 6,9e-165;
Matches 369; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

1 MYRLNRPRLPPVYMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
1 MYRLNRPRLPPVYMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACLDIYTV 120
61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACLDIYTV 120
121 HRRSL-----DSDLCIKFAMLCITLNDKCDRLK 149
121 HRRSLGNYELDVSPEDYVTSKPMKMLSKLMLKPDSDLCIKFAMLCITLNDKCDRLK 180
150 AGEACSGPHCGRHVCLRLTLFFEEKAEPHAGLLCPCAPNDRCGGERRNTIAPNCA 209
181 AGEACSGPHCGRHVCLRLTLFFEEKAEPHAGLLCPCAPNDRCGGERRNTIAPNCA 240
210 LPPVAPNCLRLCFSDPLCRSLVDVFOHCHPMDLIGTCATEOSRCLRAYIGLIGTAM 269
241 LPPVAPNCLRLCFSDPLCRSLVDVFOHCHPMDLIGTCATEOSRCLRAYIGLIGTAM 300
270 TPNFVSNVNTSVLSTCGSGNLOECCMLGEGFFSHNCLTEAIAAKRFSQLSQDM 329
301 TPNFVSNVNTSVLSTCGSGNLOECCMLGEGFFSHNCLTEAIAAKRFSQLSQDM 360
330 PHTFAVMAHONENPAVRQPWPVPSLFSCTPLILLISLM 369
361 PHTFAVMAHONENPAVRQPWPVPSLFSCTPLILLISLM 400

RESULT 4
ID W84180
AC W84180;
DE 25-MAR-1999 (first entry)
A GDNFR-alpha-related protein 3 (GRR3).
Human; glial cell line-derived neurotrophic factor receptor;
GDNFR; glial cell line-derived neurotrophic factor; GDNF;
neurturin; signal transduction; dopaminergic nerve cell;
Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
neurological disorder; diabetes; glaucoma; sensory neuron;
retinal ganglion cell degeneration; sensory neuropathy;
retinopathy; gene therapy; GDNFR-related protein 3; GRR3.
Homo sapiens.
W09854213-A2.
03-DEC-1998.
27-APR-1998; U08486.
30-MAY-1997; US-866354.
(AMGE-) AMGEN INC. PA
Fox GM, Jinn S, Wen D;
WPI; 99-080806/07.
N-PSDB: V99329.

New isolated glial cell line-derived neurotrophic factor receptors -
used to develop products for treating e.g. improperly functioning
dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
or amyotrophic lateral sclerosis
Claim 51; Fig 15; 318pp; English.
The present sequence represents a human glial cell line derived
neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3).
The protein has similar functions to GDNFR. GDNFR proteins are
functionally characterised by the ability to bind glial cell
line-derived neurotrophic factor (GDNF) and/or neurturin specifically,
and to act as part of a molecular complex which mediates or enhances

the signal transduction affects of GDNF and/or neurturin. The proteins
can be used for treating improperly functioning dopaminergic nerve
cells, Parkinson's disease, Alzheimer's disease or amyotrophic lateral
sclerosis. They can also be used for treating neurological disorders
associated with diabetes, glaucoma or other diseases and conditions
involving retinal ganglion cell degeneration, sensory neuropathy caused
by injury to, insults to, or degeneration of, sensory neurons.
The products can also be used for detection, diagnosis, drug screening
and gene therapy.
Sequence 400 AA;

Query Match 98.5%; Score 1992.5; DB 1; Length 400;
Best Local Similarity 92.0%; Pred. No. 1.5e-164;
Matches 368; Conservative 0; Mismatches 1; Indels 31; Gaps 1;

1 MYRLNRPRLPPVYMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
1 MYRLNRPRLPPVYMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACLDIYTV 120
61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACLDIYTV 120
121 HRRSL-----DSDLCIKFAMLCITLNDKCDRLK 149
121 HRRSLGNYELDVSPEDYVTSKPMKMLSKLMLKPDSDLCIKFAMLCITLNDKCDRLK 180
150 AGEACSGPHCGRHVCLRLTLFFEEKAEPHAGLLCPCAPNDRCGGERRNTIAPNCA 209
181 AGEACSGPHCGRHVCLRLTLFFEEKAEPHAGLLCPCAPNDRCGGERRNTIAPNCA 240
210 LPPVAPNCLRLCFSDPLCRSLVDVFOHCHPMDLIGTCATEOSRCLRAYIGLIGTAM 269
241 LPPVAPNCLRLCFSDPLCRSLVDVFOHCHPMDLIGTCATEOSRCLRAYIGLIGTAM 300
270 TPNFVSNVNTSVLSTCGSGNLOECCMLGEGFFSHNCLTEAIAAKRFSQLSQDM 329
301 TPNFVSNVNTSVLSTCGSGNLOECCMLGEGFFSHNCLTEAIAAKRFSQLSQDM 360
330 PHTFAVMAHONENPAVRQPWPVPSLFSCTPLILLISLM 369
361 PHTFAVMAHONENPAVRQPWPVPSLFSCTPLILLISLM 400

RESULT 5
ID W65117
AC W65117;
DE 28-SEP-1998 (first entry)
Human GDNF alpha-3 receptor protein #2.
Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;
amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
muscular dystrophy; diagnostic.
Homo sapiens.
Key
FH Key
FT Protein
EP-846764-A2.
10-JUN-1998.
20-NOV-1997; 309375.
09-MAY-1997; GB-009463.
27-NOV-1996; GB-024677.
(SMIK) SKITRKLNE BEECHAM PLC.
Lawrence GMP;
WPI; 98-29980/27.
N-PSDB: V35365.
New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
used to treat neuro degenerative diseases, muscular diseases and

Location/Qualifiers
1. 400
/label= GDNF alpha-3
/note= "partial sequence"

PT nerve and muscle trauma and in diagnostic assays
 PS Claim 13; Fig 4; 22pp; English.
 CC This sequence represents a novel glial cell line-derived neurotrophic
 CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to
 CC treat e.g. neurodegenerative diseases (such as Parkinson's disease,
 CC amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA),
 CC Huntington's Disease, Alzheimer's Disease, diabetic neuropathy,
 CC muscular diseases (including the muscular dystrophies) and nerve and
 CC muscle trauma and in diagnostic assays for such conditions.
 SQ Sequence 400 AA;

Query Match 98.4%; Score 1990.5; DB 1; Length 400;
 Best Local Similarity 92.0%; Pred. No. 2,3e-104;
 Matches 368; Conservative 0; Mismatches 1; Indels 31; Gaps 1;

QY 1 MVRPLNRPPLPPVYMLLPPSPPLAAGDPLPTESRMNSCLQARRKQADPTCSAA 60
 DB 1 MVRPLNRPPLPPVYMLLPPSPPLAAGDPLPTESRMNSCLQARRKQADPTCSAA 60
 DB 61 YHHDSCSTSSISTPLPSEEPSVPADCLAAQOLNNSLIGCMCHRRKKNQVACDIYWTW 120
 DB 61 YHHDSCSTSSISTPLPSEEPSVPADCLAAQOLNNSLIGCMCHRRKKNQVACDIYWTW 120
 QY 121 HRASSL-----DSDLCKFAMCTLNKCDRLK 149
 DB 121 HRASSLGNYELDVSPEDYTSKPKMNLSTLMLKPKPSDCLCKFAMCTLNKCDRLK 180
 QY 150 AYGEACSGPHQORHVCRLQLLTFEKAEPHAGLLCPCAPNDRGGERRRNTIAPNCA 209
 DB 181 AYGEACSGPHQORHVCRLQLLTFEKAEPHAGLLCPCAPNDRGGERRRNTIAPNCA 240
 QY 210 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDILGTCAEQSRCLRAYLGLIGTAM 269
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 QY 270 TPNFVSNVNTSVLSCRCRSGNLQEBCEMELGFFSHNPCLTEAIAKMFHSQLFSQDM 329
 DB 301 TPNFVSNVNTSVLSCRCRSGNLQEBCEMELGFFSHNPCLTEAIAKMFHSQLFSQDM 360
 QY 330 PHPTFAVMAHQNENPAVRPQWPVPSLFSCTPLPILLLSLW 369
 DB 361 PHPTFAVMAHQNENPAVRPQWPVPSLFSCTPLPILLLSLW 400

RESULT 6
 W84185
 ID W84185 standard; Protein; 378 AA.
 W84185;

25-MAR-1999 (first entry)
 De Glial cell line-derived neurotrophic factor receptor gamma 1;
 KW Glial cell line-derived neurotrophic factor receptor gamma 1;
 KW GDNF-alpha; glial cell line-derived neurotrophic factor; GDNF;
 KW neurodegenerative diseases; amyotrophic lateral sclerosis; GDNF-gamma1;
 KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
 KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
 KW renal disorder; kidney failure; gut dysfunction; regeneration;
 KW cardiomyocyte; epithelium; hepatocyte.
 OS Homo sapiens.
 FH key
 FT Peptide 1..31
 FT /label- signal_peptide
 FT 32..378
 FT Protein
 FT /label- mature_protein
 FT 32..360
 FT Domain
 FT /note- "extracellular domain"
 FT 361..378
 FT /note- "transmembrane domain"

MO853069-A2.
 PD 26-NOV-1998.
 PD 20-MAY-1998; U10328.
 PR 27-JUN-1997; US-884638.
 PR 20-MAY-1997; US-047092.

PA (HOMA-) HUMAN GENOME SCI INC.
 PI Gentz R, Hsu T, Ni J, Ruben SM, Young P;
 DR MPI; 99-070150/06.
 DR N-PSDB: V99333.
 PT New isolated glial cell derived neurotrophic factor receptors - used
 PT to develop products for treating e.g. neurodegenerative disorders,
 PT schizophrenia, hypertension, tumours, renal disorders, kidney
 PT failure or gut dysfunction
 PS Claim 26; Fig 4A-C; 156pp; English.
 CC The present sequence represents a glial cell line-derived neurotrophic
 CC factor receptor gamma 1 (GDNF-gamma1). GDNF-gamma1 shares high homology
 CC with GDNF-alpha, which is capable of complexing with glial cell
 CC line-derived neurotrophic factor (GDNF) and mediating cell response to
 CC GDNF. The GDNF polypeptides and agonists can be used for treating
 CC disorders associated with decreased activity of the respective
 CC polypeptides. They can be used for treating neurodegenerative diseases
 CC such as amyotrophic lateral sclerosis, Parkinson's disease,
 CC schizophrenia, insomnia, tardive dyskinesia, hypertension, pituitary
 CC adenomas, hyperprolactinemia, thyroid tumour, renal disorders, kidney
 CC failure, gut dysfunction, or for regeneration of cardiomyocytes,
 CC epithelium or hepatocytes. Antagonists of the polypeptides can be used
 CC for treating disorders associated with increased activity of the
 CC respective polypeptides. The products can also be used for detection,
 CC diagnosis and drug screening.
 SQ Sequence 378 AA;

Query Match 91.5%; Score 1849.5; DB 1; Length 378;
 Best Local Similarity 86.8%; Pred. No. 3.2e-152;
 Matches 347; Conservative 0; Mismatches 0; Indels 53; Gaps 2;

QY 1 MVRPLNRPPLPPVYMLLPPSPPLAAGDPLPTESRMNSCLQARRKQADPTCSAA 60
 DB 1 MVRPLNRPPLPPVYMLLPPSPPLAAGDPLPTESRMNSCLQARRKQADPTCSAA 60
 DB 61 YHHDSCSTSSISTPLPSEEPSVPADCLAAQOLNNSLIGCMCHRRKKNQVACDIYWTW 120
 DB 61 YHHDSCSTSSISTPLPSEEPSVPADCLAAQOLNNSLIGCMCHRRKKNQVACDIYWTW 120
 QY 121 HRASSL-----DSDLCKFAMCTLNKCDRLK 149
 DB 121 HRASSLGNYELDVSPEDYTSKPKMNLSTLMLKPKPSDCLCKFAMCTLNKCDRLK 180
 QY 150 AYGEACSGPHQORHVCRLQLLTFEKAEPHAGLLCPCAPNDRGGERRRNTIAPNCA 209
 DB 181 AYGEACSGPHQORHVCRLQLLTFEKAEPHAGLLCPCAPNDRGGERRRNTIAPNCA 240
 QY 210 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDILGTCAEQSRCLRAYLGLIGTAM 269
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 QY 270 TPNFVSNVNTSVLSCRCRSGNLQEBCEMELGFFSHNPCLTEAIAKMFHSQLFSQDM 329
 DB 301 TPNFVSNVNTSVLSCRCRSGNLQEBCEMELGFFSHNPCLTEAIAKMFHSQLFSQDM 338
 QY 330 PHPTFAVMAHQNENPAVRPQWPVPSLFSCTPLPILLLSLW 369
 DB 339 PHPTFAVMAHQNENPAVRPQWPVPSLFSCTPLPILLLSLW 378

RESULT 7
 W37462
 ID W37462 standard; Protein; 315 AA.
 AC W37462;
 DT 21-MAY-1998 (first entry).
 DE Human Ret ligand RetL3 partial sequence.
 KW Ret ligand; RetL3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;

myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN W09744356-A2.
 PD 27-NOV-1997; U07726.
 PF 07-MAY-1997; US-017427.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIOT) BIOGEN INC.
 PI Hession C, Santicola-Nadel M;
 PI Cate RL, 018631/02.
 DR N-PSDB; V00250.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells.
 PS Claim 2; Page 81-82; 113pp; English.
 This amino acid sequence comprises a human Ret ligand (RetL3)
 partial polypeptide sequence, deduced from a partial clone (see
 V00250) isolated from a human adult heart cDNA library; a
 full-length RetL3 sequence (see W37453) is also claimed, as well
 as rat and human RetL3. Human RetL2 and mouse RetL3 sequences
 (see W37455-61). Ret ligand is a key component of the Ret
 signalling pathway that specifically interacts with Ret receptor
 protein, triggering Ret dimerisation and/or autophosphorylation of
 the Ret tyrosine kinase domain. Vectors containing or transfected
 prokaryotic or eukaryotic host cells transformed or transfected
 with these vectors are claimed, as well as a method for production
 of RetL3. Its soluble variants and fusion proteins with a toxin,
 immunisable compound or radionuclide. RetL3, optionally when
 expressed from vectors in vivo, is used to promote growth of new
 tissue and survival of damaged tissue, particularly kidney or
 neural tissue. Typical applications are in renal failure,
 nephritis, kidney transplants, toxic or hypoxic injury,
 neurodegeneration, motor neuron disease, multiple sclerosis,
 bacterial, viral or prion infections (e.g. meningitis, myelopathy
 associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 spinal cord injury, developmental disorders such as Down's syndrome
 and cerebral palsy, or conditions involving the peripheral nervous
 system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 315 AA.

Query Match 74.9%; Score 1514.5; DB 1; Length 315;
 est Local Similarity 90.0%; Pred. No. 2,2e-123;
 Matches 278; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

92 QLRNSSLLIGCMCHRRKKNVACLDIYTVHARRSL----- 127
 Db 7 QLRNSSLLIGCMCHRRKKNVACLDIYTVHARRSL----- 127
 QY 127 -----DSDLCLFAMICTLNDKCDLRKAYGACGSPCHORHVCRLRLTFEKAAPH 180
 Db 127 -----DSDLCLFAMICTLNDKCDLRKAYGACGSPCHORHVCRLRLTFEKAAPH 126
 QY 67 LNMKLPDSDCLKFAIMCTLNDKCDLRKAYGACGSPCHORHVCRLRLTFEKAAPH 240
 Db 181 AAGLLCCAPNDRCGGERRRNTIAPNCALPPVAPNCLRLRCLFSDPCRSRLVDFOTH 186
 QY 127 AAGLLCCAPNDRCGGERRRNTIAPNCALPPVAPNCLRLRCLFSDPCRSRLVDFOTH 186
 Db 241 CRRMDLTCATGOSRCRAVIGLIGTAMTPNFVSNVTSVALSCIRSGNIGCECEML 300
 QY 187 CRRMDLTCATGOSRCRAVIGLIGTAMTPNFVSNVTSVALSCIRSGNIGCECEML 246
 Db 301 EGFFSHNPLCTEIAIAAKKRFHSQLEFSODMPHPTFAVMAHONENPAVPOPWPSLECTL 360
 QY 247 EGFFSHNPLCTEIAIAAKKRFHSQLEFSODMPHPTFAVMAHONENPAVPOPWPSLECTL 306
 Db 361 PLILLISLM 369
 QY 307 PLILLISLM 315

RESULT 8
 ID W84182
 DB W84182 standard; Protein; 397 AA.
 AC 25-MAR-1999 (first entry)
 DE A GDNFR-alpha-related protein 3 (GRR3).
 KW Rat; glial cell line-derived neurotrophic factor; GDNF;
 KW GDNFR; glial cell line-derived neurotrophic factor; GDNF;
 KW neurotrophin; signal transduction; dopaminergic nerve cell;
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KW neurological disorder; diabetes; glaucoma; sensory neuron;
 KW retinal ganglion cell degeneration; sensory neuronopathy;
 KW retinopathy; gene therapy; GDNFR-related protein 3; GRR3.
 OS Rattus sp.
 PN W09854213-A2.
 PD 03-DEC-1998; U08486.
 PF 27-APR-1997; US-866354.
 PR 30-MAY-1997; US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 PI WPI; 99-080806/07.
 DR N-PSDB; V99331.
 PT New isolated glial cell line-derived neurotrophic factor receptors
 PT used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 PT or amyotrophic lateral sclerosis.
 PS Claim 51; Fig 17; 318pp; English.
 The present sequence represents a rat glial cell-line derived
 CC neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3).
 CC The protein has similar functions to GDNFR. GDNFR proteins are
 CC functionally characterised by the ability to bind glial cell
 CC line-derived neurotrophic factor (GDNF) and/or neurotrophin specifically,
 CC and to act as part of a molecular complex which mediates or enhances
 CC the signal transduction affects of GDNF and/or neurotrophin. The proteins
 CC can be used for treating improperly functioning dopaminergic nerve
 CC cells; Parkinson's disease, Alzheimer's disease or amyotrophic lateral
 CC sclerosis. They can also be used for treating neurological disorders
 CC associated with diabetes, glaucoma or other diseases and conditions
 CC involving retinal ganglion cell degeneration, sensory neuronopathy caused
 CC by injury to, insults to, or degeneration of, sensory neurons, etc.
 CC pathological conditions, or disease or injury-related retinopathies.
 CC The products can also be used for detection, diagnosis, drug screening
 CC and gene therapy.
 SQ Sequence 397 AA.

Query Match 72.2%; Score 1459; DB 1; Length 397;
 Best Local Similarity 69.9%; Pred. No. 1.8e-118;
 Matches 276; Conservative 28; Mismatches 57; Indels 34; Gaps 2;

6 NPPPLPVLVIMLLLPSPPLFIAAGDPLPESRLNLSCLQARRKCOADPTCSAAYHLD 65
 Db 6 SPRLPVLVIMLLLPSPPLFIAAGDPLPESRLNLSCLQARRKCOADPTCSAAYHLD 62
 QY 66 SCSSISITPLPSEPPVAPADCELAQQLNSSLIGCMCHRRKKNVACLDIYTVHARRS 125
 Db 63 SCSSISITPLPSEPPVAPADCELAQQLNSSLIGCMCHRRKKNVACLDIYTVHARRS 122
 QY 126 L-----DSDLCLFAMICTLNDKCDLRKAYGACGSPCHORHVCRLRLTFEKAAPH 240
 Db 123 LADYLDVSPEDTVTSKPKMKMLSKLSMLKPDSDCLKFAIMCTLNDKCDLRKAYGAC 182
 QY 155 CGSPCHORHVCRLRLTFEKAAPHRAOGLLLCPCAPNDRCGGERRRNTIAPNCALPPVA 214
 Db 183 CGSPCHORHVCRLRLTFEKAAPHRAOGLLLCPCAPNDRCGGERRRNTIAPNCALPPVA 214
 QY 215 PNCLELRCLFSDPCRSRLVDFOTHCHPMOILGTCATGOSRCRAVIGLIGTAMTPNFV 274
 Db 243 PNCLELRCLFSDPCRSRLVDFOTHCHPMOILGTCATGOSRCRAVIGLIGTAMTPNFV 274
 QY 275 SNVTSVALSCIRSGNIGCECEMLBGFHNPCLTEIAIAAKKRFHSQLEFSODMPHPTF 334

DB 303 SKNTVVALGCTCRGSGNLODECEOLEKSFQNPCLMEIAAKMRHRLFSQDWDSTF 362
 QY 335 AVAAHONENPAVRPOPVPISFSCPTLPIILILSLM 369
 DB 363 SYWQOONSPALRPLQPLRPLSLFILLITLILQTLW 397

RESULT 9
 W37461
 ID W37461 standard; Protein: 397 AA.
 AC W37461, 21-MAY-1998 (first entry)
 DE Mouse Ret ligand RetL3.
 KW Ret ligand; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Mus musculus.
 PN MO9744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR N-PSDB: V00249.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2; Page 77-78; 113pp; English.
 CC This amino acid sequence comprises mouse Ret ligand (RetL3) RetL3,
 CC deduced from cDNA clones (see V00249) isolated from an EST
 CC database and by 5'RACE. Rat and human RetL3, human RetL3 and RetL3
 CC sequences (see W37457-60 and W37462-63) are also claimed. RetL3 is
 CC a key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing RetL3 DNA and prokaryotic or eukaryotic host
 CC cells transformed or transfected with these vectors are claimed, as
 CC well as a method for production of RetL3, its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL3, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue.
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 397 AA;

Query Match 72.1%; Score 1458; DB 1; Length 397;
 Best Local Similarity 70.2%; Pred. No. 2.2e-118;
 Matches 275; Conservative 29; Mismatches 56; Indels 32; Gaps 2;

QY 9 PLPPLVLTLLPLPPPLPLAGDPLPTESRLNNSCLQARKCOADPSCAAAYHHIDSC 68
 DB 7 PRPPLTLMILLIVLSLWPLDAGNSLATEFNFSCTQARKKCEANPACRAAYHIDSC 65

QY 69 SLSITPLSEEPSPADCLLEAAQOLNSSLIGCMCHRRKKNVACLDIYTWYHARSL-- 127
 DB 66 SLSITPLSEEPSPADCLLEAAQOLNSSLIDCRCHRRKKNVACLDIYTWYHARSLGD 125
 QY 127 -----DSDCLKFMCLTLDNCRDLRRAYGEACSG 157
 DB 126 YELDVSPYEDVTSKPMKMNLSKLNMLKPDSDCLKFMCLTLDNCRDLRRAYGEACSG 185
 QY 158 PHCQRNVCRLQRLTTFEEAEPHAGLLCPAPDRCCGERRNTIAPNCALPVPAPNC 217
 DB 186 IRCQRNVCRLQRLTTFEEAEPHAGLLCPAPDRCCGERRNTIAPNCALPVPAPNC 245
 QY 218 LELRLCFSPDPLCRSLVDFOFHCHPMOILGTCATEGSRCLRAYVLGTMTBPVNSV 277
 DB 246 LDRFCFADPLCRSLVDFOFHCHPMOILGTCATEGSRCLRAYVLGTMTBPVNSV 305
 QY 278 NTSVALSTCRGSGNLODECEOLEKSFQNPCLMEIAAKMRHRLFSQDWDSTF 337
 DB 306 NTSVALSTCRGSGNLODECEOLEKSFQNPCLMEIAAKMRHRLFSQDWDSTF 365
 QY 338 AHONENPAVRPOPVPISFSCPTLPIILILSLM 369
 DB 366 QOONSPALRPLQPLRPLSLFILLITLILQTLW 397

RESULT 10
 W37465
 ID W37465 standard; Protein: 346 AA.
 AC W37465;
 DE Mouse Ret ligand RetL3 partial sequence.
 KW Ret ligand; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Mus musculus.
 PN MO9744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR N-PSDB: V00256.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Disclosure: Page 73-74; 113pp; English.
 CC This polypeptide comprises a partial sequence of mouse Ret ligand
 CC RetL3, deduced from EST AA050083 cDNA (see V00256). A full-length
 CC mouse RetL3 sequence (see W37461) was also obtained. Rat, mouse
 CC and human RetL3, RetL2 and RetL3 cDNA sequences (see V00245-51) and
 CC encoded polypeptides (see W37457-63) are claimed and can be used
 CC in methods for promoting cell growth and improving survival of
 CC cells, especially renal or neural cells.
 CC Sequence 346 AA;

Query Match 62.6%; Score 1266.5; DB 1; Length 346;
 Best Local Similarity 71.8%; Pred. No. 6.5e-102;
 Matches 237; Conservative 20; Mismatches 42; Indels 31; Gaps 1;

QY 71 ISPLPSEEPSPADCLLEAAQOLNSSLIGCMCHRRKKNVACLDIYTWYHARSL---- 127
 DB 17 LSRPLPLESAMSADCLLEAAQOLNSSLIDCRCHRRKKNVACLDIYTWYHARSLDYE 76

QY 127 -----DSDLCIKFAMLCITLNDKCDRLKRAYGACSGPH 159
 DB 77 LDVSPEDYVTSKPKWKNLSKMLKPSDLCIKFAMLCITLNDKCDRLKRAYGACSGR 136
 QY 160 CORHCLGQLLFFKKAEPHAGLLCPAPNDRCGERRRNTIAPNCPAPVAPNCL 219
 DB 137 CORHCLGQLLFFKKAEPHAGLLCPAPNDRCGERRRNTIAPNCPAPVAPNCL 196
 QY 220 LRLCFSDPLCRSLVVDOTCHPMIDIGTCATEOSRCRAVLIGTGTMTNPNVSNVT 279
 DB 197 LRLCFSDPLCRSLVVDOTCHPMIDIGTCATEOSRCRAVLIGTGTMTNPNVSNVT 256
 QY 280 SVASCTCRGSGNLQEECEMLGFFSHNCLTEATAAKRHFSSOLFSODMPHPTAVMAH 339
 DB 257 TVALSCRCRSGNLQEECEMLGFFSHNCLTEATAAKRHFSSOLFSODMPHPTAVMAH 316
 QY 340 QNENPAPVPOWVPSLFCSTPLILLISIM 369
 DB 317 QNSNPALRLOPRLPILSILPILLITLM 346

RESULT 11

ID W65118 standard; Protein; 172 AA.
 AC W65118;
 DT 28-SEP-1998 (first entry)
 DE Human GDNF alpha-3 receptor protein fragment.
 KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
 KW treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
 KW Huntington's disease; Alzheimer's disease; diabetic neuropathy; muscle;
 KW muscular dystrophy; diagnostic.
 FH Homo sapiens.
 FT Key Location/Qualifiers
 FT 1..172
 FT /label= "GDNF alpha-3"
 FT /note= "Partial sequence"
 PN EP-846764-A2.
 PD 10-JUN-1998.
 PR 20-NOV-1997; 309375.
 PR 09-MAY-1997; GB-009463.
 PR 27-NOV-1996; GB-024677.
 PA (SMIRK) SMITHKLINE BEECHAM PLC.
 PI Lawrence GMP.
 DR WPI: 98-299860/27.
 N-PSDB: V35366.
 CC New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
 CC used to treat neuro degenerative diseases, muscular diseases and
 CC nerve and muscle trauma and in diagnostic assays
 PS Claim 29; Fig 6; 23pp; English.
 CC This sequence represents a fragment from a novel glial cell line-derived
 CC neurotrophic factor alpha-3 receptor (GDNF alpha-3). This protein can be
 CC used to treat e.g. neurodegenerative diseases (such as Parkinson's
 CC disease, amyotrophic lateral sclerosis (ALS), spinal muscular atrophy
 CC (SMA), Huntington's disease, Alzheimer's disease, diabetic neuropathy),
 CC muscular diseases (including the muscular dystrophies) and nerve and
 CC muscle trauma and in diagnostic assays for such conditions.
 SQ Sequence 172 AA;

Query Match 46.7%; Score 944; DB 1; Length 172;
 Best Local Similarity 100.0%; Pred. No. 2e-74;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 ERRRNTIAPNCPALPPVAPNCLERLCSFDPICRSRLVDFOTCHPMIDIGTCATEOSRC 257
 DB 1 ERRRNTIAPNCPALPPVAPNCLERLCSFDPICRSRLVDFOTCHPMIDIGTCATEOSRC 60
 QY 258 LRAVIGLIGTAMPNPNVSNVTVAALSCRCRSGNLQEECEMLGFFSHNCLTEATAAK 317
 DB 61 LRAVIGLIGTAMPNPNVSNVTVAALSCRCRSGNLQEECEMLGFFSHNCLTEATAAK 120

QY 318 MRFHSQLSQDMPHPTAVMAHONENPAPVPOWVPSLFCSTPLILLISIM 369
 DB 121 MRFHSQLSQDMPHPTAVMAHONENPAPVPOWVPSLFCSTPLILLISIM 172

RESULT 12

ID W84183 standard; Protein; 498 AA.
 AC W84183;
 DT 25-MAR-1999 (first entry)
 DE Consensus sequence of rat and human GDNF and GFR proteins.
 KW Glial cell-line derived neurotrophic factor receptor;
 KW GDNF; glial cell line-derived neurotrophic factor; GDNF;
 KW neurotrophin; signal transduction; dopaminergic nerve cell;
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KW neurological disorder; diabetes; glaucoma; sensory neuron;
 KW retinal ganglion cell degeneration; sensory neuropathy;
 KW retinopathy; gene therapy; GDNF-related protein; GFR.
 OS Synthetic.
 OS Rattus sp.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FH MISC.difference 1..498
 FT /note= "x-not specified"
 PN W09854213-A2.
 PD 03-DEC-1998.
 PR 27-APR-1998; U08486.
 PR 30-MAY-1997; US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jang S, Men D;
 DR WPI: 99-080806/07
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 PT used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 PT or amyotrophic lateral sclerosis
 PS Claim 51; Fig 19; 318pp; English.
 CC The present sequence represents a consensus sequence of rat and
 CC human glial cell-line derived neurotrophic factor receptor (GDNFR)
 CC protein and GDNFR-related (GRR) proteins. The proteins have similar
 CC functions. GDNFR proteins are functionally characterised by the ability
 CC to bind glial cell line-derived neurotrophic factor (GDNF) and/or
 CC neurotrophin specifically, and to act as part of a molecular complex which
 CC mediates or enhances the signal transduction affects of GDNF and/or
 CC neurotrophin. The proteins can be used for treating improperly functioning
 CC dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease or
 CC amyotrophic lateral sclerosis. They can also be used for treating
 CC neurological disorders associated with diabetes, glaucoma or other
 CC diseases and conditions involving retinal ganglion cell degeneration,
 CC sensory neuropathy caused by injury to, insults to, or degeneration of,
 CC sensory neurons, pathological conditions, or disease or injury-related
 CC retinopathies. The products can also be used for detection, diagnosis,
 CC drug screening and gene therapy.
 SQ Sequence 498 AA;

Query Match 28.6%; Score 579; DB 1; Length 498;
 Best Local Similarity 38.0%; Pred. No. 2.4e-42;
 Matches 141; Conservative 22; Mismatches 152; Indels 56; Gaps 10;

QY 1 MYRPLNRPPLPPVLMILLIPSPPLPLA---GDPPTSRRLMSNCLQARRRCCQADPTC 57
 DB 1 MYRPLNRPPLPPVLMILLIPSPPLPLA---GDPPTSRRLMSNCLQARRRCCQADPTC 59
 QY 58 SAAYVHLDSCTS--SISTPLPS--EESPVPADCLEAQAOLRNSSLIGCMCHRRKKNOVACL 114
 DB 60 SXXYRRLRQCAKXKXMTXLAGSEKXXXXXXKXAXEXLXSSLYOCRCRGKREKEXCL 119
 QY 115 DIYWTVA-----RARSLD-----SDLCIKRA 135
 DB 120 XIYWSKXIXLXGXNXXLEKSPYEVYTSRLSDIFRXXSXXSXXDXKXXKSNXCIDA 179
 QY 136 MCTLNDKCDRLKRAYGAC-----SGPHCRHVVCRLQLITFEKKAEPHAGLLCPA 190


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QY 69 S--SISTPLSEEPSVPADCEAAOOLNSSLIGCMCHRMKNQVACDIYTVH----- 122
DB 61 AGDRNTMLANKE-----CQAALEVLEQESPLYPDCKRCKMKEQLCQIYVSHLGLTE 114
QY 122 -----RARSIDSDLCLEFAMLCITLNDKCDRLR 148
DB 115 GEEFYEASPYEPVTSRLSDIFRLASIFSGTGTDPVSTKSNHCLDAAKACMLNDCKRLR 174
QY 149 KAVEGACS-----GPHCOHRYCLROLITFEFEKAEPHNOGLCCPANDGCGRRRNT 203
DB 175 SSTYSICNREISPEPERCKRCKHAKLROFFEDRVSEYTYRMLFCSC--QDACAERRRQT 232
QY 204 IAPNCAL-PPVAPNCLLELRCLFSDPLCRSLVDFOHCHP--MDILGTCAEQSRCLRA 260
DB 233 ILPSCSYEDKEKFPNCILDRSLCRTDHLCRSLADPHANCRASYRTITSCPADNTQACIGS 292
QY 261 YLGLIGTAMTPNFVSNVNTSVALS--CTCRGSGNLQECCEMLGEGFFSHNPCLTEAIAA 316
DB 293 YAGMIGEDMTPNYVDSNPTGIYVSPMCNCRSGNMEECEKFLDFTENPCILRNAIQA 350

RESULT 15
ID W71604 standard: Protein; 664 AA.
AC W71604;
DE 19-NOV-1998 (first entry)
KW Human; neurturin receptor alpha; NTNR-alpha; variant; chimeric;
   fusion protein; immunoadhesion; ret-expressing cell; neurological;
   renal; haematological disease.
OS Synthetic.
OS Homo sapiens.
OS Rattus sp.
PN MO9836072-A1.
PD 20-AUG-1998.
PE 17-FEB-1998; 003179.
PR 24-OCT-1997; US-957063.
PR 18-FEB-1997; US-802805.
PR 09-JUN-1997; US-871913.
PA (GENTH ) GENENTECH INC.
PI Hynes MA, Klein KD, Rosenthal A;
DR WPI: 98-467175/40.
PT N-PSDB; V58007.
PT New polypeptide(s) based on human neurturin receptor alpha and
   ret-expressing cells for treating e.g. neurological, renal and
   haematological diseases
   Example 3; Page 84-86; 116pp; English.
CC The present sequence represents rat neurturin receptor alpha
   (NTNR-alpha)/Fc sequence (IFF2a) fusion protein, from an example of the
   present invention. NTNR-alpha proteins can be used: (a) to identify
   molecules that bind specifically to it (potential agonists and
   antagonists) and to purify such compounds; (b) to modulate response of
   cells or to activate Ret on the surface of cells (soluble glial derived
   neurotrophic factor receptor (GDNFR alpha) may be used the same way);
   (d) to increase the half-life of cognate ligands (especially NTN); (e)
   diagnostically to determine serum levels of its ligands; and (f) as
   animal feed additive or molecular weight marker. NTNR-alpha, its genes,
   (ant)agonists and antisense nucleic acids, are useful in vivo or ex vivo
   for treating conditions related to abnormal NTN activity or response,
   particularly neurological (central or enteric), renal or haematopoietic
   (spleen) diseases or injuries. Ab may be agonists or antagonists for
   therapeutic use (e.g. as antagonists to treat excessive/unwanted NTNR-
   alpha expression, e.g. in some tumours), also reagents for immunoassay
   and affinity purification.
SQ Sequence 664 AA:

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Query Match      25.4%; Score 514; DB 1; Length 664;
Best Local Similarity 35.3%; Pred. No. 1.4e-36;
Matches 114; Conservative 38; Mismatches 113; Indels 58; Gaps 8;

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QY 44 CLOARRCOADPTCSAAYHHHDSTS--SISTPLSEEPSVPADCEAAOOLNSSLIGC 101
DB 40 CVRAMEICAAESSNCSNRYRTLRQCLAGDRNTMLANKE-----CQAALEVLEQESPLYDC 93
QY 102 MCHRRMKNOVACDIYTVH-----RA 123
DB 94 RCKRGMKELOCLOIYVSHGLTEGEEFYEASPYEPVTSRLSDIFRLASIFSGTGDPA 153
QY 124 RSLSDLCLEFAMLCITLNDKCDRLRKAYGACS-----GPHCOHRYCLROLITFEFEKAEL 178
DB 154 VSTRSNHCLDAKACMLNDCKRLRSSYISICNREISPEPERCKRCKHAKLROFFEDRVPS 213
QY 179 PHAGLLCPCAPNDRCGERRRNTIAPNCAL-PPVAPNCLLELRCLFSDPLCRSLVD 237
DB 214 EYTYRMLFCSC--QDACAERRRQTILPSCSYEDKEKFPNCILDRSLCRTDHLCRSLADF 271
QY 238 QTHCHP--MDILGTCAEQSRCLRAYLGLTAMTPNFVSNVNTSVALS--CTCRGSGNL 293
DB 272 HANCRASYRTITSCPADNTQACIGSYAGMIGEDMTPNYVDSNPTGIYVSPMCNCRSGNM 331
QY 294 QEECEMLEGFFSHNPCLTEAIAA 316
DB 332 EEECEKFLDFTENPCILRNAIQA 354

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Search completed: December 13, 1999, 02:27:10
Job time: 440 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:19:33 ; Search time 33.26 Seconds

(Without alignments)
736.683 Million cell updates/sec

Title: US-09-272-835-15

Perfect score: 2199

Sequence: 1 MVRPLNRPRLPPVYMLLL.....PWVPSLFSCTLPILLISIM 400

Scoring table: BLOSUM62

Searched: 199794 seqs, 61255205 residues

abase :

SPTREMBL_11:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp Vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2187	99.9	400	4	060609	060609 homo sapien
2	1646.5	75.2	397	11	035118	035118 mus musculu
3	1643.5	75.0	397	11	055243	055243 mus musculu
4	1641.5	75.0	397	11	035325	035325 mus musculu
5	542.5	24.8	464	11	035977	035977 rattus norv
6	540.5	24.7	464	4	015316	015316 homo sapien
7	540.5	24.7	464	4	015328	015328 homo sapien
8	517.5	23.6	460	4	015507	015507 homo sapien
9	516	23.6	465	4	043912	043912 homo sapien
10	514.5	23.5	463	11	035252	035252 mus musculu
11	513	23.4	468	11	035246	035246 mus musculu
12	512.5	22.7	463	13	035748	035748 rattus norv
13	497.5	22.4	431	13	035512	035512 gallus gall
14	418.5	19.1	358	11	092283	092283 mus musculu
15	408	18.6	330	11	092282	092282 mus musculu
16	147	6.7	2704	5	097458	097458 diosophila
17	133.5	6.1	2653	5	025253	025253 lucilia cup
18	123.5	5.6	2195	5	020462	020462 caenorhabd
19	122.5	5.5	3857	11	088840	088840 mus musculu
20	120	5.5	1964	11	035442	035442 mus musculu
21	115	5.3	850	4	095804	095804 homo sapien
22	115	5.3	876	11	088799	088799 mus musculu
23	114	5.2	1999	4	099940	099940 homo sapien
24	114	5.2	2003	4	099466	099466 homo sapien
25	114	5.2	955	4	099466	099466 homo sapien
26	114	5.2	1034	11	003488	003488 rattus norv
27	113.5	5.0	2026	4	000468	000468 homo sapien
28	109.5	5.0	949	5	P90956	P90956 caenorhabd
29	109	5.0	580	4	000634	000634 homo sapien

30	108.5	5.0	4545	11	061291	061291 mus musculu
31	108	4.9	989	4	094909	094909 homo sapien
32	107	4.9	1598	5	094438	094438 chironomus
33	107	4.9	1792	13	057484	057484 gallus gall
34	106	4.8	473	5	025464	025464 mytilus gall
35	104	4.7	2352	11	061240	061240 halocynthia
36	104	4.7	1203	11	006008	006008 mus musculu
37	104	4.7	2470	11	035516	035516 mus musculu
38	103	4.7	2150	5	044131	044131 caenorhabd
39	102.5	4.7	1581	13	073809	073809 fugu rubrip
40	101.5	4.6	1681	5	077244	077244 chlorohydra
41	101	4.6	1077	3	074853	074853 schizosacch
42	100	4.6	2408	4	092566	092566 homo sapien
43	100	4.6	1513	5	017970	017970 caenorhabd
44	100	4.6	1254	13	09YH02	09YH02 brachydanio
45	98.5	4.5	468	13	09Y195	09Y195 rana rugosa

ALIGNMENTS

RESULT 1

060609 ID 060609 PRELIMINARY; PRT; 400 AA.

AC 060609; 01-ANG-1998 (TREMBLrel. 07, Created)

DT 01-ANG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-ANG-1998 (TREMBLrel. 07, Last annotation update)

DE GDNF FAMILY RECEPTOR ALPHA 3.

GN GFR3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RA BALCH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L., FOPPESTON C., JOHNSON E.M., JR., MILLBRAND J., 5/98

RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).

DR EMBL: AF051767; AAC24355.1; --

SQ SEQUENCE 400 AA; 44538 MW; 6DFB5381 CRC32;

Query Match	99.9%	Score 2187;	DB 4;	Length 400;
Best Local Similarity	99.8%	Pred. No. 3.6e-214;		
Matches 399;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	MVRPLNRPRLPPVYMLLLLPSPPLAAGDPLPTESRLMNSCLQARRCOADPTCSAA	60		
DB 1	MVRPLNRPRLPPVYMLLLLPSPPLAAGDPLPTESRLMNSCLQARRCOADPTCSAA	60		
QY 61	YHLDCTSSISTPLPSEPSYPADCLERAQGLRNSSLIGCMCHRRMKNOVACLDIYTV	120		
DB 61	YHLDCTSSISTPLPSEPSYPADCLERAQGLRNSSLIGCMCHRRMKNOVACLDIYTV	120		
QY 121	HRASLGNELVSPEDVYTSKPMKMLSKPMKPSDCLTKAMCTLDKCDRLRK	180		
DB 121	HRASLGNELVSPEDVYTSKPMKMLSKPMKPSDCLTKAMCTLDKCDRLRK	180		
QY 181	AYGACSGPHCRHVCRLRLTFFEKAAEPHAQGLLCPCAENDGCGERRRNTAPNCA	240		
DB 181	AYGACSGPHCRHVCRLRLTFFEKAAEPHAQGLLCPCAENDGCGERRRNTAPNCA	240		
QY 241	LEPVAPNCELELRCLFSDPLCRSLVDFOHCPMDIIGTCATGESCRLRAYLIGITAM	300		
DB 241	LEPVAPNCELELRCLFSDPLCRSLVDFOHCPMDIIGTCATGESCRLRAYLIGITAM	300		
QY 301	TENFVSNTVTSVALSCTCGSGNLOECGEMLEGFSHPNCLTEATAARKRFSSQSDW	360		
DB 301	TENFVSNTVTSVALSCTCGSGNLOECGEMLEGFSHPNCLTEATAARKRFSSQSDW	360		
QY 361	PAPTFAVAHONENPAVRPOPVVPSLFSCTLPILLISIM 400			
DB 361	PAPTFAVAHONENPAVRPOPVVPSLFSCTLPILLISIM 400			

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RESULT 2
ID 035118 PRELIMINARY; PRT: 397 AA.
AC 035118;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE GLIAL CELL LINE DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA 3
DE (GFRALPHA-3).
GN GFR3 OR GFRALPHA-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL6; TISSUE-HEART;
RX MEDLINE; 98205811.
RA NOMOTO S., ITO S., YANG L.-X., KIUCHI K.;
Molecular cloning and expression analysis of GFR alpha-3, a novel
cDNA related to GDNF alpha and NTR alpha.;
Biochem. Biophys. Res. Commun. 244:849-853(1998).
RN 171
RP SEQUENCE FROM N.A.
RA BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,
RA POBESCU N.C., JOHNSON E.M. JR., MIBRANDT J.;
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).
DR EMBL; AB008833; BAA23562.1;
DR EMBL; AF051766; AAC24354.1;
DR MGI; MGI:1201403; GFR3.
SQ SEQUENCE 397 AA; 44307 MW; A80EDD24 CRC32;

Query Match 75.28; Score 1646.5; DB 11; Length 397;
Best Local Similarity 77.8%; Pred. No. 2,7e-159;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

OY 9 PLPPVLMILLLPSPPLAAGDPLPTESRLNSCLQARRKCOADPTCSAAVYHLLDSC 68
DB 7 PRPP-LMLILLVLSLWPLDAGNSLATERFVNSCTQARRKCAAPACKAAVOHLGSC 65
OY 69 SSISTPLPSEEPVADCLLEAQQQLNSLIGCMCHRRKQVACLDIYTWVHARSIGN 128
DB 66 SLSPLPSEASMSADCLLEAQQQLNSLIGCMCHRRKQVACLDIYTWVHARSIGN 125
OY 129 YELVSPEDVTYTSKPMKNTSKLMLKPPSDLCLEFAMCTLNDKCDRLKAYGEACSG 188
DB 126 YELVSPEDVTYTSKPMKNTSKLMLKPPSDLCLEFAMCTLNDKCDRLKAYGEACSG 185
OY 189 PHGRHCLRLTLFEFEKAEPHAGLLCPCAPNDKCGGRRNTIAPNCALPVPAPNC 248
DB 186 IRCRHHCLLQKRFFEEKAESHAGLLCPCAPNDKCGGRRNTIAPNCALPVPAPNC 245
OY 249 LELRLCFSPDLCSRLVDFOTCHPMIDLGTCATEOSRCLRAVLGLIGTAMPNFEVSNY 308
DB 246 LDRSFCADPLCSRLMDPOTCHPMIDLGTCATEOSRCLRAVLGLIGTAMPNFEVSNY 305
OY 309 NTSVALSCTCGSGNLOECECEMLEGFFSHNPLCTEAIARHFSOLFSDWPHPTFAVM 368
DB 306 NTSVALSCTCGSGNLOECECEMLEGFFSHNPLCTEAIARHFSOLFSDWPHPTFAVM 365
OY 369 AHONENPAVRPQWPVPSLFTPLILLISLW 400
DB 366 QQONSFPALRLOPRLPILSIFLILLQTLW 397.

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DT 01-JUN-1998 (Tremblrel. 06, Last annotation update)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA WIDENFALK J., TOMAC A., LINDQVIST E., HOFER B., OLSON L.;
Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN 121
RP SEQUENCE FROM N.A.
RA NAVEITHAN P., BAUDERT C., MIKAELS O., SHEN L., WESTPHAL H.,
RA ERNFORS P.;
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).
DR EMBL; AF041842; AAC23558.1;
DR EMBL; AF036163; AAC24468.1;
SQ SEQUENCE 397 AA; 44302 MW; F77607CF CRC32;

Query Match 75.0%; Score 1643.5; DB 11; Length 397;
Best Local Similarity 77.0%; Pred. No. 5.5e-159;
Matches 305; Conservative 31; Mismatches 59; Indels 1; Gaps 1;

OY 5 LNRPPLPVLMILLLPSPPLAAGDPLPTESRLNSCLQARRKCOADPTCSAAVYHLL 64
DB 3 LSLEPRPP-LMLILLVLSLWPLDAGNSLATERFVNSCTQARRKCAAPACKAAVOHL 61
OY 65 DSCSSISTPLPSEEPVADCLLEAQQQLNSLIGCMCHRRKQVACLDIYTWVHARS 124
DB 62 GSCSSISRLPSEASMSADCLLEAQQQLNSLIGCMCHRRKQVACLDIYTWVHARS 121
OY 125 SLGNYELVSPEDVTYTSKPMKNTSKLMLKPPSDLCLEFAMCTLNDKCDRLKAYGE 184
DB 122 SLGNYELVSPEDVTYTSKPMKNTSKLMLKPPSDLCLEFAMCTLNDKCDRLKAYGE 181
OY 185 ACSGPCORHVCRLQTLFEFEKAEPHAGLLCPCAPNDKCGGRRNTIAPNCALPVP 244
DB 182 ACSGPCORHVCRLQTLFEFEKAEPHAGLLCPCAPNDKCGGRRNTIAPNCALPVP 241
OY 245 APNCLELRCLFSDPLCSRLVDFOTCHPMIDLGTCATEOSRCLRAVLGLIGTAMPN 304
DB 242 TPNCLELRCLFSDPLCSRLVDFOTCHPMIDLGTCATEOSRCLRAVLGLIGTAMPN 301
OY 305 VSNVNTVALSCTCGSGNLOECECEMLEGFFSHNPLCTEAIARHFSOLFSDWPHPT 364
DB 302 VSNVNTVALSCTCGSGNLOECECEMLEGFFSHNPLCTEAIARHFSOLFSDWPHPT 361
OY 365 FAVMHONENPAVRPQWPVPSLFTPLILLISLW 400
DB 362 FSVYQOONSFPALRLOPRLPILSIFLILLQTLW 397

RESULT 4
ID 035325 PRELIMINARY; PRT: 397 AA.
AC 035325;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-AUG-1998 (Tremblrel. 07, Last annotation update)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA TROPP M., RAYNOSCHER C., IBANEZ C.F.;
Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF020305; AAB70931.1;
SQ SEQUENCE 397 AA; 44333 MW; F0C0C841 CRC32;

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Query Match 75.0%; Score 1641.5; DB 11; Length 397;
 Best Local Similarity 77.6%; Pred. No. 8.8e-159;
 Matches 304; Conservative 30; Mismatches 57; Indels 1; Gaps 1;

DB 9 PLPPVATMLLLPLPSPLPLAAGDPLPESRLMNSQLARRKCOADPTCSAAVHHLSDCT 68
 7 PRPP-ILMILLILSLMPLPLGAGNSLNTATNFRVNSCTQARRKCEANPACKAYOHLSGCT 65
 69 SSIPTPLSEPSVADCLLEAAQOLNSSLICGCHRRKKNVACLDIYTVHARRSLGN 128
 66 SLSPLPLESAMSADCLLEAAQOLNSSLIDRCRRKKNVACLDIYTVHARRSLGN 125
 129 YELDVSPEDVTSKPMKNSKLMKLPDSDCLKFMALCTLNKCORLRAVGEACSG 188
 126 YELDVSPEDVTSKPMKNSKLMKLPDSDCLKFMALCTLNKCORLRAVGEACSG 185
 189 PHCRHVCRLQLTEFFEKAAEPHAGLLCPAPNDRCGERRRTIAPNCALPVAFNC 248
 186 IRCORHLCAGRSFEKAAESHAGLLCPAPNDRCGERRRTIAPNCALPVAFNC 245
 249 LELRLCTSDPLCSRLVDFTCHGHPDILGTGATGOSRCLRAYLGLTANTPVFVNV 308
 246 LELRLCTSDPLCSRLVDFTCHGHPDILGTGATGOSRCLRAYLGLTANTPVFVNV 305
 309 NTVALCTCGSGNLOECCEMLGEGFSHNPCLTEAIAKKRHSOLSPHPTFAVM 368
 306 NTVALCTCGSGNLOECCEMLGEGFSHNPCLTEAIAKKRHSOLSPHPTFAVM 365
 369 AHQENPAVPPQVWVPSLFCSTPLILLSLM 400
 366 QOQNSNPALRLQPLRLPLSLILLILLM 397

RESULT 5
 035977 PRELIMINARY; PRT; 464 AA.

ID 035977; PRELIMINARY; PRT; 464 AA.
 AC 035977;
 DT 01-JAN-1998 (TEMBREL. 05, Last sequence update)
 DT 01-JAN-1998 (TEMBREL. 05, Last sequence update)
 DT 01-AUG-1998 (TEMBREL. 11, Last annotation update)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA (GDNF RECEPTOR-BETA).
 GN GDNF-BETA OR RETL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.
 [1]
 SEQUENCE FROM N.A.
 TRUMP M., RAYNOSCHER C., IBANEZ C.F.;
 Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 [2]
 SEQUENCE FROM N.A.
 TISSUE-BRAIN/KIDNEY;
 MEDLINE; 97322356.
 RA SANICOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C., WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A., PEPINSKY R.B., CATE R.L.;
 Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 [4]
 SEQUENCE OF 1-444 FROM N.A.
 TISSUE-HIPOCAMPUS;
 SUVANTO P., WATTIOVAARA K., LINDAHL M., MOSHAYAROV M., ARDUE U., HORELLI-KUITUNEN N., AIRAKSINEN M.S., PALOTIE A., SAARA M.;
 Cloning, mRNA distribution and chromosomal localization of the gene

RT for glial cell line-derived receptor beta, a homolog to
 RT GDNF-alpha;
 RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF005226; AAB62247.1;
 DR EMBL; U97143; AAC53301.1;
 DR EMBL; AF003825; AAD09310.1;
 KW Receptor.
 SO SEQUENCE 464 AA; 51668 MW; B1A2BD11 CRC32;

Query Match 24.8%; Score 542.5; DB 11; Length 464;
 Best Local Similarity 37.4%; Pred. No. 4.1e-47;
 Matches 123; Conservative 42; Mismatches 125; Indels 39; Gaps 10;

DB 44 CLOARRKCOADPTCSAAVHHLSDCT--SISTPLSEPSVADCLLEAAQOLNSSLICG 101
 40 CYRANELCAESNCSRRITRQCLAGDRNTMLANKE-----COALEVLQSSPLYDC 93
 102 MCHRRKNQVACLDIYTVHARRSLGNVELDVSPEDVTSKPMKNSKLMKLPDSDCL 156
 94 RCKRGMKKELOCLQIYMSHGLGEGEFYEASPYE-PVTSR-----LSDIFRLASIFSG 147
 156 -----KPSDCLKFMALCTLNKCDRLKRAYGEACS-----GPHCRHVCRLQLLT 203
 148 TGTPPAVSTSNHCLDAKACNTLNDCKRLSSYISICNREISPTERCNRKCHKALROF 207
 204 FEKAEPHAGLLCPAPNDRCGERRRTIAPNCAL-PPVAPNCLERLCFSPDLR 262
 208 FDRPSETYRMLFCSC--ODQCAERKROTILPSCSYEDKERNCLDLSLRTHLCR 265
 263 SRLVDFTCHGHP--MDILGTGATGOSRCLRAYLGLTANTPVFVNVVNTVALS--CTC 318
 266 SRLADFANCRASYRITISCPADNYQACLSYAGMIGFDMTPVYDSNPFQIYVSRNC 325
 319 RGSNLOECCEMLGEGFSHNPCLTEAIAA 347
 326 RGSNMEDECEKFLRPTENPCLNMAIOA 354

RESULT 6
 015316 PRELIMINARY; PRT; 464 AA.

ID 015316; PRELIMINARY; PRT; 464 AA.
 AC 015316;
 DT 01-JAN-1998 (TEMBREL. 05, Last sequence update)
 DT 01-JAN-1998 (TEMBREL. 05, Last sequence update)
 DT 01-AUG-1998 (TEMBREL. 07, Last annotation update)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR BETA.
 GN GDNF-BETA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 [1]
 SEQUENCE FROM N.A.
 TISSUE-FETAL BRAIN;
 RA WARTIOVAARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL M., MOSHAYAROV M., AIRAKSINEN M.S., PALOTIE A., SANICOLA M., SUVANTO P., WATTIOVAARA K., LINDAHL M., MOSHAYAROV M., ARDUE U., HORELLI-KUITUNEN N., AIRAKSINEN M.S., PALOTIE A., SAARA M.;
 Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U93703; AAB61922.1;
 SO SEQUENCE 464 AA; 51530 MW; DE80D543 CRC32;

Query Match 24.7%; Score 540.5; DB 4; Length 464;
 Best Local Similarity 36.5%; Pred. No. 6.6e-47;
 Matches 120; Conservative 47; Mismatches 123; Indels 39; Gaps 10;

DB 44 CLOARRKCOADPTCSAAVHHLSDCT--SISTPLSEPSVADCLLEAAQOLNSSLICG 101
 40 CYRANELCAESNCSRRITRQCLAGDRNTMLANKE-----COALEVLQSSPLYDC 93
 102 MCHRRKNQVACLDIYTVHARRSLGNVELDVSPEDVTSKPMKNSKLMKLPDSDCL 153
 94 RCKRGMKKELOCLQIYMSHGLGEGEFYEASPYE-PVTSR-----LSDIFRLASIFSG 147


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DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-AUG-1998 (Tremblrel. 07, Last annotation update)
DE GPI-LINKED ANCHOR PROTEIN.
DE GPR1.
SN Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC Euthelia; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA ANGRIST M., JING S., BOLK S., BENTLEY K., NALLASAMY S., HALUSHKA M.,
RA FOX G.M., CHAKRAVARTI A.;
RA Genomics 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-MEDULLARY THYROID CARCINOMA TUMOR;
RC SHEPHERDINE S.E., KHORANA S., SCHULTZ P.N., HUANG E., THOBE N.,
HU Z.J., FOX G.M., JING S., COTE G.J., GAGEL R.F.;
Hum. Genet. 0:0-0(1998).
DR EMBL: AF038420; AAC39693.1; JOINED.
DR EMBL: AF038411; AAC39693.1; JOINED.
DR EMBL: AF038412; AAC39693.1; JOINED.
DR EMBL: AF038413; AAC39693.1; JOINED.
DR EMBL: AF038414; AAC39693.1; JOINED.
DR EMBL: AF038415; AAC39693.1; JOINED.
DR EMBL: AF038416; AAC39693.1; JOINED.
DR EMBL: AF038417; AAC39693.1; JOINED.
DR EMBL: AF038418; AAC39693.1; JOINED.
DR EMBL: AF038419; AAC39693.1; JOINED.
DR EMBL: AF042080; AAB97371.1; JOINED.
DR EMBL: AF038421; AAC39692.1; JOINED.
DR EMBL: AF058899; AAC14431.1; JOINED.
DR EMBL: AF058890; AAC14431.1; JOINED.
DR EMBL: AF058891; AAC14431.1; JOINED.
DR EMBL: AF058892; AAC14431.1; JOINED.
DR EMBL: AF058893; AAC14431.1; JOINED.
DR EMBL: AF058894; AAC14431.1; JOINED.
DR EMBL: AF058895; AAC14431.1; JOINED.
DR EMBL: AF058896; AAC14431.1; JOINED.
DR EMBL: AF058897; AAC14431.1; JOINED.
DR EMBL: AF058898; AAC14431.1; JOINED.
SQ SEQUENCE 465 AA; 51455 MW; 1C4EAE03 CRC32;

Query Match 23.6%; Score 516; DB 4; Length 465;
Best Local Similarity 36.3%; Pred. No. 2e-44;
Matches 131; Conservative 45; Mismatches 133; Indels 52; Gaps 13;
17 LLLLLPPSPPLA---GDLPTESRLMNSCLARRCQADPTCSAAYHLDSCS---70
6 LYPALPLDLILLSEVSGGDRL-----DCVKAPOCKLEQSCSKRYRLRCVAGKE 57
70 ---SISTLPSEBSVPADCLAAQOLRNSLIGCMCHRRKKNVACLDIYTVHARSLS 126
58 TNSLSASGLAKD---ECRSAMEALKOKSLYNCRCRKGKKKKELRIYWSYQSLQ- 112
127 GNYELDVSPYEDVTYSKPMKMLSKLNLKP-DSDL-----CLKFAMLCYLD 173
112 GNDLLEDSPE-----PVNSRLSDIFRVPFISDVYQVYEHIPKGNKNCIDAKACNLDD 165
174 KCPRLKAYEAC---SGPHCORHVCRLRLTFEERKAEPHAOGILLCPAPNDRCGCE 229
166 ICKKYSAYTTPCTTSVSNVNCNRKCHKALROFDKVPKHSYGMFCSC--RDICTE 223
230 RRRNTAPNCLP-VAPNCLERLCFSDPLCRSLYVDQTHCPMD-ILGTCATEQ-S 286
224 RRRQTVPCSYEREKRPCLNLODSCKTYICRSRLADFTNCOPESSRSVSSCLKENYA 283
287 RCLRAYLGLIGTAMTPEFVSNTVSTVALSCTCRGSGNLOECCMLEGFFSHNCLTEAIA 346
284 DCLLAASGLIGTAMTPEFVSNTVSTVALSCTCRGSGNLOECCMLEGFFSHNCLTEAIA 343
QY 347 A 347

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DB 344 A 344

RESULT 10
ID 035252 PRELIMINARY; PRT; 463 AA.
AC 035252;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JAN-1998 (Tremblrel. 05, Last annotation update)
DE GDNF RECEPTOR BETA.
DE GDNFR-BETA.
GN GDNF-BETA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthelia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL Neuroreport 9:0-0(0001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF015172; AAB86600.1; JOINED.
SQ SEQUENCE 463 AA; 51134 MW; 910EF17F CRC32;

Query Match 23.5%; Score 514.5; DB 11; Length 463;
Best Local Similarity 36.1%; Pred. No. 2.9e-44;
Matches 128; Conservative 46; Mismatches 136; Indels 45; Gaps 12;
14 VMLLLLLPPSPPLAAGDPLPTESRLMNSCLARRCQADPTCSAAYHLDSCS---70
9 VLPDLIDLSA--EVSGGDRL-----DCVKAPOCKLEQSCSKRYRLRCVAGKE 58
70 ---SISTLPSEBSVPADCLAAQOLRNSLIGCMCHRRKKNVACLDIYTVHARSLS 127
59 NFSLTSGLEAKD---ECRSAMEALKOKSLYNCRCRKGKKKKELRIYWSYQSLQ-G 112
128 NYELDVSPYEDVTYSKPMKMLSKLNLKP-----DSDLCLKFAMLCYLDKCDRLR 179
113 NDLLLEDSPE-----PVNSRLSDIFRVPFISDVYQVYEHIPKGNKNCIDAKACNLDDTCKYR 166
180 KAYGEAC---SGPHCORHVCRLRLTFEERKAEPHAOGILLCPAPNDRCGERRRNTI 235
167 SAYITPCTTSMSNEVCNRKCHKALROFDKVPKHSYGMFCSC--RDVACTERRQTI 224
236 APNCLP-VAPNCLERLCFSDPLCRSLYVDQTHCPMD-ILGTCATEQ-SRCLRAY 292
225 VPVCSYEEREPCLNLODSCKTYICRSRLADFTNCOPESSRSVSSCLKENYADCLL 284
293 LGLIGTAMTPEFVSNTVSTVALSCTCRGSGNLOECCMLEGFFSHNCLTEAIA 347
285 SGLIGTAMTPEFVSNTVSTVALSCTCRGSGNLOECCMLEGFFSHNCLTEAIA 339
DB 285 SGLIGTAMTPEFVSNTVSTVALSCTCRGSGNLOECCMLEGFFSHNCLTEAIA 339

RESULT 11
ID 035246 PRELIMINARY; PRT; 468 AA.
AC 035246;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JAN-1998 (Tremblrel. 05, Last annotation update)
DE GDNF RECEPTOR ALPHA.
GN GDNFR-ALPHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthelia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-C57; TISSUE-LIVER;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL NeuroReport 9:0-0(0001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57; TISSUE-LIVER;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF014117; AAB86599.1;
SQ SEQUENCE 468 AA; 51751 MW; AFDCE6A1 CRC32;

Query Match 23.4%; Score 513; DB 11; Length 468;
Best Local Similarity 36.1%; Pred. No. 4.1e-44;
Matches 130; Conservative 46; Mismatches 134; Indels 50; Gaps 13;

QY 14 VLMLLLPPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAYHHLDSTCS--- 70
DB 9 VLPLDLMLSA--EVSGGDRL-----DCVKSADQCLKEQSCSTYRTLRQCVACKET 58
DU 70 --SISTPLPSEPSVPADCLAAQOLNSSLIGCMCHRRKNQVACIDIVYTHARASLG 127
DU 59 NFSLTSLGKAD-----ECRSAMEALOKSLYNCRCRKGKKKCNCLRIYWSYQSLQ-G 112
QY 128 NYELDVSPYEDVTYKPKMKNLSKLNKLP-DSDL-----CLKFAMLCITLNDK 174
DB 113 NDLEDSPE-----PVNSRLSDIFRAVPFISDVFOQVEHISGNNCCLDAACACINDDT 166
QY 175 CDRLKRAYGEAC---SGPHCORHVLCRLQLTFEKAEPHAQGLLPCAPNDRGGER 230
DB 167 CKYRSAYITPCTSMNSNENCNKCKKALROFFDKYPAHSGMLFCSC--RDVACTER 224
QY 231 KRTIAPNCLLP-VAPNCLRLRCLFSDPLCRSLVDFTQHPMD-ILGTCTEAO-SR 287
DB 225 RROTIYVPCSEYERERENCINLQDCKTNYICRSRLADFPTNCOPESRSVSNCKENYAD 284
QY 288 CLRAYGLISTAMTPNVSVMNTSVALSCTCRSGSNLQCECEMLEGFFSHNPLCTEALIA 347
DB 285 CLAYSGLISTAMTPNVTSSLSVAPWCDCSNSSGNDLECLAFNFKDNTCLKNAIOA 344

RESULT 12

035748 PRELIMINARY; PRT; 463 AA.

AC 035748; 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, last sequence update)
DL 01-JAN-1998 (TREMblrel. 05, last annotation update)
GDNF-ALPHA/TRMR1-DELTA PROTEIN.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HANNOVER;
RA ZHONG J., ANNES M., HEIMANN R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: A002072; CAA05171.1;
SQ SEQUENCE 463 AA; 51032 MW; 93377F91 CRC32;

Query Match 23.4%; Score 512.5; DB 11; Length 463;
Best Local Similarity 36.0%; Pred. No. 4.6e-44;
Matches 128; Conservative 44; Mismatches 137; Indels 47; Gaps 12;

QY 17 LLLPLPSPPLA---GDPLTESRLMNSCLQARRKQADPTCSAAYHHLDSTCS--- 70
DB 6 LVFALPLDLMLSAEYSGDRL-----DCVKSADQCLKEQSCSTYRTLRQCVACKET 57
QY 70 ----SISTPLPSEPSVPADCLAAQOLNSSLIGCMCHRRKNQVACIDIVYTHARASL 126
DB 58 TNSLTSLGKAD-----ECRSAMEALOKSLYNCRCRKGKKKCNCLRIYWSYQSLQ- 112

QY 127 GNYELDVSPYEDVTYKPKMKNLSKLNKLP-----DSDCLKFAMLCTLNDKDR 178
DB 112 GNDLEDSPE-----PVNSRLSDIFRAVPFISVHISGNNCCLDAACACINDDTCKKY 165
QY 179 KRAYGEAC---SGPHCORHVLCRLQLTFEKAEPHAQGLLPCAPNDRGGERRRNT 234
DB 166 RRAYITPCTSMNSNENCNKCKKALROFFDKYPAHSGMLFCSC--RDVACTERROT 223
QY 235 IAPNCLLP-VAPNCLRLRCLFSDPLCRSLVDFTQHPMD-ILGTCTEAO-SRCLRA 291
DB 224 IYVPCSEYERERENCINLQDCKTNYICRSRLADFPTNCOPESRSVSNCKENYADCL 283
QY 292 YLIGISTAMTPNVSVMNTSVALSCTCRSGSNLQCECEMLEGFFSHNPLCTEALIA 347
DB 284 YSLIGISTAMTPNVTSSLSVAPWCDCSNSSGNDLECLAFNFKDNTCLKNAIOA 339

RESULT 13

093512 PRELIMINARY; PRT; 431 AA.

AC 093512; 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, last sequence update)
DE GFR RECEPTOR ALPHA 4 PRECURSOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98313402.
RA THOMPSON J., DOXAKIS E., PINON L.G., STRACHAN P., BUT-BELLO A.,
RA WYATT S., BUCHMAN V.L., DAVIES A.M.,
RT "GFRalpha-4, a new GDNF family receptor."
RL Mol. Cell. Neurosci. 11:117-126(1998).
DR EMBL: AF045162; AAC36464.1;
KW signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 431 AA; 47964 MW; 7AE1F0B0 CRC32;

Query Match 22.7%; Score 497.5; DB 13; Length 431;
Best Local Similarity 34.8%; Pred. No. 1.4e-42;
Matches 111; Conservative 37; Mismatches 148; Indels 23; Gaps 8;

QY 44 CLARRKQADPTCSAAYHHLDSTCSISTPLPSEPSVPADCLAAQOLNSSLIGCMC 103
DB 26 CLAGESTNDPICSCKFTLRQCLIA--GNGANKLGPAKNGCRSTYVALLSQLYGCKC 83
QY 104 HRKMNQVACIDIVYTHARASLGNYELDVSPYEDVTYKPKMKNLSKLNKLPDSD--- 161
DB 84 KRGKKEKHCHLSVYVSIHTLTMEGNVLESSEPEYFING---FDYVRLASTAGSENEY 139
QY 151 ----CLKFAMLCITLNDKDRKRAYGEAC---SGPHCORHVLCRLQLTFEKAEPHA 211
DB 140 TVYNCLDAARACNDVEMCGRLRTYVSCIRRLARADTCRCKKALRKFFDVPPPEY 199
QY 212 AAGLLCPCAPNDRGGERRRNTIAPNCL-PPVAPNCLRLRCLFSDPLCRSLVDFTQ 270
DB 200 THELFPCPC--EDVACARROTIVPACSYSEKERNCLAPLDSRENYVCRSRYAEQF 257
QY 271 HCHP-NDLGTCTEAO-SRCLRAYIGLIGTAMTPNVSVMNTSVALSCTCRSGSNLQCEC 328
DB 258 NQPSLQTSACRNDSTYACLAATYTGILGSPITPYIDNSTSIAPWCTCNASGNRODEC 317
QY 329 EMLGEFFSHNPLCTEALIA 347
DB 318 ESFLHFTDNVCCLONALIOA 336

RESULT 14

0922A3

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 12, 1999, 19:58:52 ; Search time 27.76 seconds

(without alignments)
679.673 Million cell updates/sec

Title: US-09-272-835-15

Sequence: 1 MVRPLNPRLPPVVMILL.....PWVPSLFSCTPLILLISLM 400

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database:

PIR_62: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1646.5	75.2	397	2 JE0082	GPI-linked receptor
2	147	6.7	2703	1 A24420	notch protein - fr
3	133.5	6.1	3084	1 MMSA	laminin alpha-1 ch
4	124	5.7	1700	2 S08167	Balbiani ring 3 pr
5	123.5	5.6	3002	2 A47221	fibrillin 1 precu
6	123.5	5.6	2871	2 A55567	fibrillin 1 - bov
7	120	5.5	1964	2 T09059	notch - mouse
8	117.5	5.4	2704	2 S09118	G surface protein
9	116	5.3	3635	2 T10053	laminin alpha 5 ch
10	115	5.3	2531	2 A46019	Notch-1 protein -
11	114.5	5.2	2871	2 A55624	fibrillin-1 precu
12	114	5.2	2531	2 S18188	notch protein homo
13	114	5.2	1034	2 J05598	mucin - rat
14	112.5	5.1	4543	1 A53102	alpha-2-macroglobu
15	112.5	5.1	2535	1 A40043	notch protein homo
16	111.5	5.1	1609	1 MMSB2	laminin gamma-1 ch
17	111.5	5.1	1106	2 T13938	gene shuttle craft
18	110	5.0	4544	1 S02392	alpha-2-macroglobu
19	110	5.0	2321	2 S78549	notch3 protein - h
20	109	5.0	2139	2 A35672	alpha-2-macroglobu
21	108.5	5.0	4545	1 S25111	G surface protein
22	108	4.9	2718	2 A23475	adhesive plaque pr
23	106	4.8	2918	2 A54105	laminin gamma-1 ch
24	106	4.8	473	2 A56175	coagulation factor
25	105	4.8	1607	1 MMSB2	laminin alpha-1 ch
26	105	4.8	1959	1 AGRT	agrin - rat
27	105	4.8	593	2 S45281	laminin alpha-1 ch
28	105	4.8	3075	2 S14458	fibrillin-2 precu
29	105	4.8	2907	2 A57278	laminin gamma-1 ch
30	104	4.7	1639	1 MMSB2	granulin precursor
31	104	4.7	593	1 CYHR	cell-fate determin
32	104	4.7	2471	2 A49128	Notch B protein -
33	104	4.7	1203	2 A49175	Notch 3 protein -
34	103.5	4.7	384	2 S25771	probable vitelloge
35	102.5	4.7	2318	2 S45306	acetylcholinester
36	100.5	4.6	1984	2 T13171	deoxyribonuclease
37	99.5	4.5	591	1 S55632	hypothetical prote
38	98	4.5	509	1 S55632	
39	98	4.5	1808	2 T15099	

40 97.5 4.5 540 2 BA7417 Insulin receptor-T
41 97.5 4.5 996 2 JE0237 apolipoprotein E r
42 97.5 4.5 589 2 C38128 epithelin/granulin
43 97 4.4 833 2 S19087 gene delta protein
44 97 4.4 754 2 S17063 fibrillin (clone M
45 96.5 4.4 4753 1 A47437 LDL-receptor-relat

ALIGNMENTS

RESULT 1
JE0082
GPI-linked receptor precursor - mouse
N:Alternate names: GFRalpha-3
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 17-Mar-1999
C:Accession: JE0082
R:Nomoto, S.; Ito, S.; Yang, L.X.; Kirsch, K.
BIOCHEM. BIOPHYS. Res. Commun. 244, 849-853, 1998
A:Title: Molecular cloning and expression analysis of GFRalpha-3, a novel CDNA related
A:Reference number: JE0082; MUID:98205811
A:Accession: JE0082
A:Molecule type: mRNA
A:Residues: 1-397 <NOM>
A:Cross-references: DDB:AB008833; NID:G2627159; PID:G2627160
C:Comment: This protein plays a distinct role in cell survival and differentiation.
C:Keywords: glycoprotein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:380-397/Region: hydrophobic
F:92,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.2%; Score 1646.5; DB 2; Length 397;
Best Local Similarity 77.8%; Pred. No. 5.4e-123;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 9 PLPPVVMILLPLPPPLPLAGDPLPTESRLNLSCLQARRKQADPTCSAAYHHLDSC 68
DB 7 PRPP-LMILLIVLSLWPLPLAGNSLATENFVNSCTQARRKCANPACRAAYOHLSCT 65

QY 69 SSISPLPSEEPSPADCLPEAOLRNSSLICGCHRMNOVACLDITYTVHARSLGN 128
DB 66 SSIRPPLPESASACLEAEOLRNSSLIDCCHRMHQATCTDITYTVHARSLGN 125

QY 129 YELDVSPYEDVYTSKPKMNLKMLKPPSDCLKFAMLCTLNDKCDRLKAYGACSG 188
DB 126 YELDVSPYEDVYTSKPKMNLKMLKPPSDCLKFAMLCTLNDKCDRLKAYGACSG 185

QY 189 PHCRHYCLKQLTFEKAAPPAAGLLCPAPNDRCGERRRNTIAPNCALPPVAPNC 248
DB 186 IRCRHLCLQLRSEFEKAESHAGLLCPAPEDGCGERRRNTIAPNCALPPVAPNC 245

QY 249 LELRLCFSDPLCRSLVYDQTHCHPMDITGATCSRLRAYLGITGAMPNRYSVN 308
DB 246 LDLSFRADPLCRSLMDQTHCHPMDITGATCSRLRAYLGITGAMPNRYSVN 305

QY 309 NTSVALCTCRGSGNLQEECEMLEGFFSHNPLCTEAIAAKRRHSOLFSDMHPFAYV 368
DB 306 NTVVALCTCRGSGNLQEECEMLEGFFSHNPLCTEAIAAKRRHSOLFSDMHPFAYV 365

QY 369 AHQENPAPVPPQWVPSLFSCTPLILLISLM 400
DB 366 QQONSNPALRLOPRLPLTFSIPLILLISLM 397

RESULT 2
A24420
notch protein - fruit fly (Drosophila melanogaster)
N:Alternate names: neurogenic repetitive locus protein
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A24420; A24768; S09358; A05267;

R:Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A:Reference number: A24420; MUID:87064624
A:Accession: A24420
A:Molecule type: DNA
A:Residues: 1-2703 <KID>
A:Cross-references: GB:K03508; NID:g157991; PIDN:AAA28725.1; PID:g157993
R:Marion, K.A.; Johnson, K.M.; Xu, T.; Altavanni-Tsakonas, S.
Cell 43, 567-581, 1985
A:Reference number: A24768; MUID:86079539
A:Accession: A24768
A:Molecule type: mRNA
A:Residues: 1-48, 'I', '50-118', 'R', '120-230', 'I', '232-256', 'N', '258-266', 'A', '268-872', 'R', '874-958',
A>Note: The authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
R:Taute, D.
Nucleic Acids Res. 17, 6463-6471, 1989
A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA ma
A:Reference number: S09358; MUID:89385974
A:Accession: S09358
A:Molecule type: DNA
A:Residues: 2505-2551, 'Q', '2552-2576', 'E', '2578-2604 <TAU>
Marion, K.A.; Yedobnick, B.; Finnerty, V.G.; Altavanni-Tsakonas, S.
Cell 40, 55-62, 1985
A:Title: opa: a novel family of transcribed repeats shared by the Notch locus and other
A:Reference number: A05267; MUID:8509329
A:Accession: A05267
A:Molecule type: DNA
A:Residues: 2504-2576, 'E', '2578-2611 <WHA2>
C:Genetics:
A:Gene: notch; opa
A:Cross-references: FlyBase:Pg00004647
A:Map position: 8.96-9.36
A:Intons: 53/3; 84/3; 171/3; 240/3; 283/3; 233/3; 2436/3; 2588/3
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: differentiation; tandem repeat; transmembrane protein
F:27-43/Domain: transmembrane #status predicted <TM1>
F:97-128/Domain: EGF homology <EGF1>
F:330-561/Domain: EGF homology <EGF1>
F:568-599/Domain: EGF homology <EGF1>
F:988-1019/Domain: EGF homology <EGF2>
F:1064-1095/Domain: EGF homology <EGF3>
F:1187-1218/Domain: EGF homology <EGF3>
F:1746-1782/Domain: transmembrane #status predicted <TM2>
F:1950-1982/Domain: ankyrin repeat homology <AN1>
F:1983-2015/Domain: ankyrin repeat homology <AN2>
F:1988-2004/Domain: transmembrane #status predicted <TM3>
F:2017-2049/Domain: ankyrin repeat homology <AN3>
F:2050-2082/Domain: ankyrin repeat homology <AN4>
F:2083-2115/Domain: ankyrin repeat homology <AN5>
F:2358-2568/Region: glutamine-rich
F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 6.7%: Score 147; DB 1; Length 2703;
Best Local Similarity 21.9%; Pred. No. 0.0014;
Matches 86; Conservative 38; Mismatches 146; Indels 122; Gaps 23;

QY 41 MNSCLARRRCQADPTCSAAYHLDCTSSISPL-----PSEPSVPADCLBAQAQ 92
DB 985 INCLTS--GFCNGATCS--QVNSYCT-----CPLEFSQINCTNDECTESSCLANGGSC 1037
QY 93 L-----RNSLIGCMCHRMKNQVACLDIYTVH----- 122
DB 1038 IDGINSYNSCLAGYSGANCQYLNCDSPCLNGATCHEQ--NNEYTC-----HCPG 1089
QY 122 -RARSIGNT--LDVSPYEDTVSKPMKNLKLNLKLPDSDC-----L 163
DB 1090 FTGQCGSEYDNGCGSCPEGATCSQKHOFSCKSGAGTGRKCDVQITSCDPAADRKL 1149
QY 164 KFMALCTLNDKCDRLKAVGEA-----CS-----GPHCRHY-----CLRLTLF 203
DB 1150 SLMLQCN-NQTC-----KDGNSHVCCSGGYSAGSYQKKEIDECQSPQNGGICRDLJA 1204

QY 204 EKAAPPHAG-----LILPCAPN--DRG--CGERRNTIAPNCAIPVAPNCL-ELRR- 254
DB 1205 YEGCGAGGCGGCGCGLNIDDCANPNCGNGTCHDRANF---SCSPGPMGICELIND 1261
QY 254 -----LCFSDPLCRSLVDFQTHCHPMIDILGTGATEQSCLRAYTGLICTAMPNFVS 308
DB 1262 DCRPGACHNNGSCIDRVGFEVCQPGFVGARCEGIDINCLSPGCSNAGLDCVQLVNNY 1321
QY 309 NTSVALSCRGSGNQLQDECEMLEGFFSHNPG 340
DB 1322 H-----CNCR-PGHMGRCEHRKVDCAQSPC 1346

RESULT 3
MMSA
Laminin alpha-1 chain precursor - mouse
N:Alternate names: Laminin chain A1
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 16-Jul-1999
C:Accession: A31771; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670
J:Sasaki, M.; Kleiman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.
J. Biol. Chem. 263, 16536-16544, 1988
A:Title: Laminin, a multidomain protein. The A chain has a unique globular domain and
A:Reference number: A31771; MUID:89034134
A:Accession: A31771
A:Molecule type: mRNA
A:Residues: 1-3084 <SAS>
A:Cross-references: EMBL:040064; NID:g309419; PIDN:AAA39410.1; PID:g309420
A:Accession: A30449
A:Molecule type: Protein
A:Residues: 183-195; 570-571, 'A', '573-586; 596-612, 'X', '614-617, 'EMK', '630-646; 1217-1222, '2486; 2624-2639; 2818-2843; 3009-3033, 'V', '3035 <SA2>
R:Hartl, L.; Oberbauer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A:Title: The N terminus of laminin A chain is homologous to the B chains.
A:Reference number: S00624; MUID:88225080
A:Accession: S00624
A:Molecule type: mRNA
A:Residues: 1-208, 'T', '210-334 <HAR>
A:Cross-references: EMBL:X07737; NID:g52857; PIDN:CAA30561.1; PID:g52858
A:Accession: A30450
A:Molecule type: Protein
A:Residues: 311-335, 'N', '337-339; 630-642, 'D', '644; 692-734; 737-748, 'X', '750-760, 'G', '762-73-1389; 1449-1459 <HA2>
A>Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-
R:Man, K.; Deutzmann, R.; Timpl, R.
Eur. J. Biochem. 178, 71-80, 1988
A:Title: Characterization of proteolytic fragments of the laminin-nidogen complex and
A:Reference number: S08895; MUID:89078415
A:Accession: S08895
A:Molecule type: protein
A:Residues: 153-169 <MAN>
R:Fujitawa, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A:Title: Structure and distribution of N-linked oligosaccharide chains on various dom
A:Reference number: S02678; MUID:88326259
A:Accession: S02678
A:Molecule type: protein
A:Residues: 630-642, 'D', '644; 2690-2704 <FUD>
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbauer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A:Title: Structural study of long arm fragments of laminin. Evidence for repetitive C
A:Reference number: S01790; MUID:89030693
A:Accession: S01790
A:Molecule type: mRNA
A:Residues: 2538-3084 <DEU>
A:Cross-references: EMBL:X14459; NID:g55499; PIDN:CAA31807.1; PID:g818014
A:Accession: A30451
A:Molecule type: protein
A:Residues: 1911-1929; 1997-2006; 2033-2045, 'X', '2047-2054, 'X', '2056-2066, 'X', '2068-2105; 2470; 2487; 2498; 2502-2545; 2538-2557; 2561-2591, 'X', '2593-2594; 2600-2610; 2616-2645; 2648-2653; 2698-3005, 'A', '3007-3033, 'V', '3035; 3068-3083 <DE2>
A>Note: 2256-Val was also found

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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:41:35 ; Search time 20.22 seconds

(without alignments)
575.390 Million cell updates/sec

Title: US-09-272-835-15

Perfect score: 2190

Sequence: 1 MVRPLNRPRLPVVLMILL.....PWPSLSFSLPLILLSLM 400

Scoring table: BLOSUM62

Searched: 80000 seqs, 29085965 residues

Abase: SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	568	25.9	NRTR_CHICK	013157 gallus gall
2	544.5	24.9	NRTR_MOUSE	008642 mus musculu
3	540.5	24.7	NRTR_HUMAN	000451 homo sapien
4	536.5	24.5	NRTR_CHICK	013156 gallus gall
5	533	23.4	NRTR_MOUSE	097785 mus musculu
6	511	23.1	NRTR_RAT	062997 rattus norv
7	505.5	23.1	NRTR_HUMAN	056159 homo sapien
8	147	6.7	NRTR_MOUSE	P07207 drosophila
9	133.5	6.1	NRTR_MOUSE	P19137 mus musculu
10	124	5.7	NRTR_MOUSE	003336 chironomus
11	123.5	5.6	NRTR_BOVIN	P98133 mus musculu
12	123.5	5.6	NRTR_HUMAN	P35555 homo sapien
13	120	5.5	NRTR_MOUSE	P31695 mus musculu
14	117.5	5.4	NRTR_MOUSE	P17053 paramecium
15	116	5.3	NRTR_MOUSE	061001 mus musculu
16	115	5.3	NRTR_MOUSE	001705 mus musculu
17	114.5	5.2	NRTR_MOUSE	061554 mus musculu
18	114	5.2	NRTR_MOUSE	007008 rattus norv
19	112.5	5.1	NRTR_CHICK	P98157 gallus gall
20	112.5	5.1	NRTR_MOUSE	P46531 homo sapien
21	111.5	5.1	NRTR_HUMAN	P11047 homo sapien
22	111.5	5.1	NRTR_HUMAN	P40798 drosophila
23	110	5.0	NRTR_HUMAN	007954 homo sapien
24	109	5.0	NRTR_MOUSE	P10040 drosophila
25	108	4.9	NRTR_MOUSE	P13837 paramecium
26	106	4.8	NRTR_HUMAN	P33556 homo sapien
27	105	4.8	NRTR_HUMAN	P25304 rattus norv
28	105	4.8	NRTR_BOVIN	P98140 bos taurus
29	105	4.8	NRTR_MOUSE	P61555 mus musculu
30	105	4.8	NRTR_HUMAN	P25591 homo sapien
31	105	4.8	NRTR_MOUSE	P02468 mus musculu
32	104	4.7	NRTR_MOUSE	P28799 homo sapien
33	103.5	4.7	NRTR_HUMAN	001721 mus musculu
34	102.5	4.7	NRTR_MOUSE	P61982 mus musculu
35	102.5	4.6	NRTR_MOUSE	P98163 drosophila
36	100	4.6	NRTR_MOUSE	P15153 drosophila
37	99.5	4.5	NRTR_MOUSE	P28797 caria porce
38	98	4.5	NRTR_HUMAN	P98164 homo sapien
39	97	4.4	NRTR_HUMAN	Q21313 caenorhabd1
40	96.5	4.4	NRTR_MOUSE	Q04833 caenorhabd1
41	96	4.4	NRTR_MOUSE	P14585 caenorhabd1
42	95.5	4.4	NRTR_MOUSE	P61483 mus musculu
43	95.5	4.4	NRTR_HUMAN	P98155 homo sapien

ALIGNMENTS

RESULT	ID	NRTR_CHICK	STANDARD	PRT	465 AA
AC	013157				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	11-DEC-1998 (Rel. 37, Last annotation update)				
DE	NEUTRURIN RECEPTOR ALPHA PRECURSOR (NRTR-ALPHA) (NRTR-ALPHA) (GDNF RECEPTOR BETA) (GDNFR-BETA).				
GN	GPR2 OR GDNFR.				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.				
RN	SEQUENCE FROM N.A.				
RP	TISSUE-BRAIN;				
RC	MEDLINE: 97336104.				
RA	BUT-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,				
RA	ROSENTHAL A., CHINCHEIRO M., BUCHMAN V.L., DAVIES A.M.;				
RT	"Neurturin responsiveness requires a GPI-linked receptor and the Ret receptor tyrosine kinase."				
RL	Nature 387:721-724 (1997).				
CC	- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTR-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE RECEPTOR (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.				
CC	- SIMILARITY: BELONGS TO THE GDNFR FAMILY.				
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CC	EMBL: U90542; AAB61571.1;				
DR	Receptor; glycoprotein; GPI-anchor; Membrane; Signal.				
KW	SIGNAL				
FT	CHAIN				
FT	PROPEP				
FT	CARBOHYD				
FT	CARBOHYD				
FT	LIPID				
SO	SEQUENCE				
Query Match	25.9%	Score 568;	DB 1;	Length 465;	
Best Local Similarity	35.2%	Pred. No. 2.6e-39;			
Matches 136;	Conservative 50;	Mismatches 150;	Indels 50;	Gaps 13;	
DB	19	LILPSPPLPLAGDPLPES	-----RLMNSCLARRKCOADPCSAHYHDSCTS	--SIS 72	
DB	20	LAAPSP	-----PGDDLOGWVPYDCIANLCAAGSCSSRIPTLRCLLGRDRN	70	
DB	73	PLPSESPVPLDCLAAQOLNSSLIGCMCHRRKNQVACDIWTVHRAKSLGNYELD		132	
DB	71	TYLANKE	-----COAALEVLOESPLDCKRGRKREICLOVWWSHLGAEEYE	124	
DB	133	VSPYEDVTSKPKWKNLSLNL	-----KPDDELCKFAMLTDLNDKCDRLKA	181	
DB	125	ASPYE-PLTSR	-----LSDIFRLASIFSGMDPATNSKSNHCLDAKACNLNDNCRRLRS	178	


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QY 182 YGACG-----GPHCRHNCRLRLTFEKAAPHAGLILCPACANDRGERRNTIA 236
DB 179 YISTCKEISATERRCHRRKALROFEDVNPSEYTRILFCSC--KDQACAEPRROIV 236
QY 237 PNCAL-PPVAPNCLERLRCFSDPLCRSLVNDQTHCH--PMDLGTCAGAEQ--SRCLRAL 293
DB 237 PCISYDKEKPNCLDLRNCVCRADHLRSLRADHANCAQSPFSLTSCPDNTQACIGSYT 296
QY 294 GLIGTAMTENVSVNNTSVALS--CTCRGSGNLQECCEMLEGFFSHNPLCTEAIKXMF 351
DB 297 GLIGFDMTENVYDASTTSLTSPSCSKSGNLSECECFMDFTENPCLRAIQAIFGNG 356
QY 352 HSGLSQDNPHPTFAVMAHONENPAV 377
DB 357 TDVNLSPKNPSPPTIMLPYKERSPAL 382

RESULT 2
NRR_MOUSE STANDARD: PRT: 463 AA.
008842:
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
(GDNFR-BETA).
GN GFRA2 OR GDNFRB OR TRNR2.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97325791.
RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
RA HECKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
RA JOHNSON E.M. JR., MILBRANDT J.;
RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling
through Ret."
RL Neuron 18:793-802(1997).
CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NTRN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET TYROSINE KINASE
CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CERVICAL AND DORSAL
CC ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEEN
CC AND IN THE ADRENAL.
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF002701; AAC53548.1; -
CC DR MGD; MG1:1195462; GFR2.
CC KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal;
CC Alternative splicing.
CC FT SIGNAL 1 21
CC FT CHAIN 22 443
CC FT PROPEP 444 463
CC FT CARBOHYD 52 52
CC FT CARBOHYD 357 357
CC FT CARBOHYD 413 413
CC FT LIPID 443 443
CC GPI-ANCHOR (POTENTIAL).

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FT VARSPLIC 14 146 MISSING (IN SHORT FORM).
SQ SEQUENCE 463 AA; 51598 MW; 0A2165C0 CRC32;
Query Match 24.9%; Score 544.5; DB 1; Length 463;
Best Local Similarity 35.7%; Pred. No. 2,16-37;
Matches 131; Conservative 48; Mismatches 141; Indels 47; Gaps 13;
QY 44 CLQARKQADPTGSAAHVHDSCTS--SISTPLSEPSVPADCLAAQOLRNSSLIGC 101
DB 40 CVRAEILCAASNCSSRRRTLROCLAGDRNTMLANKE-----QQAILEVQESPLDQC 93
QY 102 MCHRRKNVACLDITVYVHARSIGNELDVSPEDVTSKPMNLSKL----- 153
DB 94 RCKRMKELOCLQITVSHIGLIEGEFTYASPE-PTVSR-----LSDIFRLASIFSG 147
QY 153 ----NMLKPSDCLKFAMLCTLNDKCDRLKAVGEACS-----GPHCRHNCRLRLTF 203
DB 148 TGADPVYSAKSNHCLDAKACNLNDCKKLRSYSISICNREISPTERRNRRKCHRALQF 207
QY 204 FEKAEPHAGLILCPACANDRGERRRNTIAPCAL-PPVAPNCLERLRCFSDPLCR 262
DB 208 FDRVPSEYTYMLFCSC--QDQACAEPRROIVLPCSEYDEKPKCLDLRSLCRTLHLR 265
QY 263 SRLVDFOTCHP--MDLGTGATGOSRCLRAYLLGIGAMPNPNVSNVNTSVALS--CTC 318
DB 266 SRLADFPANCASTRITISCPADNYOACLGSTYAMIGDMTPNTVDSNPIGIVVSPMCNC 325
QY 319 RGSNGLQECCEMLEGFFSHNPLCTEAIKXMFISOLFSDMPH-PTFAVMAHONENPAV 377
DB 326 RGSNMEBECEKFKDPTENCLRNAIOA---FONGDVNNSPGPIFSA-----TOAPRV 378
QY 378 RPOWMP 384
DB 379 EKTPSLP 385

RESULT 3
NRR_HUMAN STANDARD: PRT: 464 AA.
ID NRR_HUMAN
AC 000451;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
DE (GDNFR-BETA).
GN GFRA2 OR GDNFRB OR TRNR2.
OS Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97325791.
RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
RA HECKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
RA JOHNSON E.M. JR., MILBRANDT J.;
RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling
through Ret."
RL Neuron 18:793-802(1997).
CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NTRN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET TYROSINE KINASE
CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
CC SPLICING IN BOTH BRAIN AND PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
CC -----
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 CC -----
 DR EMBL: AF002700; AAC52036.1; -
 DR MIM: 601956; -
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal;
 KM Alternative splicing.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 444 NEURURIN RECEPTOR ALPHA.
 FT PROPEP 445 464 HYDROPHOBIC, REMOVED DURING MATURATION
 FT CARBOHYD 52 52 (POTENTIAL).
 FT CARBOHYD 357 357 (POTENTIAL).
 FT CARBOHYD 413 413 POTENTIAL.
 FT LIPID 444 444 GPI-ANCHOR (POTENTIAL).
 FT VASPLIC 14 146 MISSING (IN SHORT FORM).
 FT SEQUENCE 464 AA; 51558 MW; 3C74BBFB CRC32;
 Query Match 24.7%; Score 540.5; DB 1; Length 464;
 Best Local Similarity 36.5%; Pred. No. 4,5e-37;
 Matches 120; Conservative 47; Mismatches 123; Indels 39; Gaps 10;
 QY 44 CLOARRKQADPTCSAAYHNDSCTS--SISTPLPSEEPSVPADCLEAQAOLRNSLLIC 101
 DB 40 CVRAMELCAESNCSSRYTLNOCLAGRNTMLANKE-----CQALEVQDESPLYDC 93
 QY 102 MCHRRKNQVACLDITWTVHARSLGNELDYSPYEDTYSKPMKNLSKL----- 153
 DB 94 RCKRMKKELOCIQIYWSIHGLTEGEFEYEASPYE-PYTSR-----LSDIFRLASIFSG 147
 QY 153 ---MLKPSDLCKFAFLCTLNKCDLRAKYGACS-----GPHCRHYCROLLTF 203
 DB 148 TGADPVSNAKSHCHDAACACNLNDCKRLSSYSISICNREISPERCNRKCHALROF 207
 QY 204 FEKAEPHAQGLLPCAPANDRCGERRRNTIAPNCAI-PVYAPNCELELRCLFSPDLOR 262
 DB 208 FDRVSEYTYRLFFSC--QDQACAEARRQITLIPSCSYDKEKPNCLDRGVCRDHLOR 265
 QY 263 SRLVDFOHCHP--MDLIGTCATEQSRCIRAYLGLIGTAMDPNFSNVNTSYALS--CTC 318
 DB 266 SRLADFHNCRASYOTVTSAPADNTQACISYAGMIGFMETNYDSSPTGIVSPWCSC 325
 QY 319 RGSGLQECCELEGFESHNPCLTEAIAA 347
 DB 326 RSGNMEECCEKFLRDTFENPCLRNAIOA 354
 RESULT 4
 GDNF_CHICK STANDARD: PRT; 469 AA.
 ID GDNF_CHICK
 AC 013156;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-ALPHA) (TGF-BETA RELATED
 DE NEUROTROPHIC FACTOR RECEPTOR 1).
 GN GFRAL OR GDNFRA.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 CC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 AC MEDLINE; 97336104.
 RA BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,
 RA ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.,
 RT "Neurin responses requires a GPI-linked receptor and the Ret
 RT receptor tyrosine kinase."
 RL Nature 387:721-724(1997).
 CC -I- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED

CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -I- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
 CC (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE GDNF FAMILY.
 CC -----
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 CC -----
 DR EMBL: U00541; AAB61570.1; -
 DR Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
 KM Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 469 HYDROPHOBIC, REMOVED DURING MATURATION
 FT CARBOHYD 62 62 (POTENTIAL).
 FT CARBOHYD 163 163 (POTENTIAL).
 FT CARBOHYD 346 346 (POTENTIAL).
 FT CARBOHYD 405 405 (POTENTIAL).
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 FT SEQUENCE 469 AA; 52043 MW; C8D241C9 CRC32;
 Query Match 24.5%; Score 536.5; DB 1; Length 469;
 Best Local Similarity 37.2%; Pred. No. 9,7e-37;
 Matches 132; Conservative 44; Mismatches 140; Indels 39; Gaps 12;
 QY 16 MLLLLPSPPLIAG--DPLPESRLNMSCLOARRKQADPTCSAAYHNDSCTS----- 70
 DB 5 LLYLALPLADVLLSLKESVGLPGDRL--DQVAKSDQCKECSCTKYKTLNOCYAGKESN 62
 QY 70 -SISTPLPSEEPSVPADCLEAQAOLRNSLLIGCMCHRRKNQVACLDITWTVHARSLGN 128
 DB 63 FSRATGLAKD-----EKSAMEALKQSLNCRCKRMKKEKCLRTIYMSYLSLO-GN 116
 QY 129 YELDVSPYEDTYSKPMKNLSKLMLKP-----DSDCLKFAMLCITLNDKDLR 179
 DB 117 DLLEDSPYE-----PVNSRLSDIFRLAIVSEVPYLSKGNCCDAKACALNNTCRFR 170
 QY 180 KAYGAC-----SGPHCRHYCROLLTFFEKAEPHAQGLLPCAPANDRCGERRRNTI 235
 DB 171 SAYTTPCSTSTNEICNRKCHKALRLEFDVPPKHSIGMLFCSC--RDVACRERRQTI 228
 QY 236 APNCAIAP-VAPNCELELRCLFSDPLCRSLVDFOHCHPMD-ILGTCATEQ--SRCIRAY 292
 DB 229 VPVCSYEDREKPNCLNLOESCKKNYICRSRLADFTTCQPSRSVSCLENTADCLLAY 288
 QY 293 LGLIGTAMDPNFSNVNTSYALSCTCRGSGNLOECCEMLEGFESHNPCLTEAIAA 347
 DB 289 SGLIGTAMDPNFSNVNTSYALSVAPEMDCNSGNDIDECRKLNFEDNNTCLNNAIOA 343
 RESULT 5
 GDNF_MOUSE STANDARD: PRT; 468 AA.
 ID GDNF_MOUSE
 AC P97785;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-ALPHA) (TGF-BETA RELATED
 DE NEUROTROPHIC FACTOR RECEPTOR 1).
 GN GFRAL OR GDNFRA OR TRNRL.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-DORSAL ROOT GANGLION;
 RA WATABE K.;
 CC Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB000800; BAA19185.1;
 DR MGD; MGI:1100842; GPR1.
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 468 HYDROPHOBIC, REMOVED DURING MATURATION
 FT (POTENTIAL).
 FT DOMAIN 362 369 THR-RICH.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 347 347 POTENTIAL.
 FT CARBOHYD 406 406 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 SQ SEQUENCE 468 AA; 51782 MW; 6C64C182 CRC32;
 Query Match 23.4%; Score 513; DB 1; Length 468;
 Best Local Similarity 36.1%; Pred. No. 8e-35;
 Matches 130; Conservative 46; Mismatches 134; Indels 50; Gaps 13;
 QY 14 VMLLLPSPPLAAGDPLPTESRLMNSCLARRCQADPTCSAAYHLDSTS---- 70
 DB 9 VLPDLILMSA--EVSQGDRL-----DCVKNASDQLEQSCSTYKTLRCCVAKKET 58
 QY 70 --SISTPLPSEEPSPVPAQCLEAAQOLNNSLIGCMCHRMKNQVACDIYTVHARSIG 127
 59 NFSLSGLEAND-----ECRSAMEALNKGSLYNCRCKRGMKKEKNCIRITWMSQSLQ-G 112
 QY 128 NYELDVPYEDYVSKPWKNLKLNLAKP-DSPL-----CLKFAMLCTLNDR 174
 DB 113 NDLEDEPYE-----EVNSRLSDIFRAVPISDFEQVEHISGNCLDAANAACNLDIT 166
 QY 175 CDRLKRYAGEAC-----SGPHCORHVCRLRLTFPEKAAEHAQGLICPCAPNDROGGER 230
 DB 167 CKKRSAYIIPCTISMENVCNKRCKKALROTFDKVPKPAHSGMLCSC--RDVACTER 224
 QY 231 RRTIADNCALPP-VADNCLERLRCFSDPLCRSLVDFOTHCPMD-IIGTCATEQ-SR 287
 DB 225 RROTIYVVCSEYERERENCLNLDSCIKYICSRSLADFTTNOQERSRVSNLKENYAD 284
 QY 288 CLRAYIGLITAMTPNPNVSNVSYALSCRCRSGNLOECCEMLKEGFFSHNPLTEIAIA 347
 DB 285 CLAYISGLISTVMTPTNIDSSLSVAPWCSCNSNDLEDCFLFLNFFKDNLTCLAKNAIQ 344

RESULT 6
 GDNF-RAT
 ID GDNF-RAT STANDARD; PRT; 468 AA.
 AC 062957;
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-ALPHA) (TGF-BETA RELATED
 GN NEUROTROPHIC FACTOR RECEPTOR 1) (RET LIGAND 1).
 GN GPR1 OR GDNFRA OR TRNR1 OR RETL1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-RETINA;
 RX MEDLINE; 96270513.
 RA JING S., WEN D., HU Y., HOLST P.L., LEO Y., FANG M., TAMIR R.,
 RA ANTONIO L., HU Z., COPPLES R., LOUIS J.-C., HU S., ALTHROCK B.W.,
 RA FOX G.M.;
 RT "GDNF-induced activation of the ret protein tyrosine kinase is
 RT mediated by GDNF- α , a novel receptor for GDNF."
 RL Cell 85:1113-1124(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MISTAR; TISSUE-KIDNEY;
 RX MEDLINE; 97322356.
 RA SANICOLA M., HESSION C.A., MORLEY D.S., CARMILO P., EHRENFELS C.,
 RA WATUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PERINSKI R.B., CAPE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 RT can be mediated by two different cell-surface accessory proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96273032.
 RA TREANOR J.J.S., GOOGAN L., DE SAVAGE F., STONE D.M., POULSEN K.T.,
 RA BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HEFTI F.,
 RA PHILLIPS H.S., GODDARD A., MOORE M.N., BUT-BELLO A., DAVIES A.M.,
 RA ASAI N., TAKAHASHI M., VANDLEN R., HENDERSON C.E., ROSENTHAL A.;
 RT "Characterization of a multicomponent receptor for GDNF."
 RL Nature 382:80-83(1996).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
 CC -1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U59486; AAC52663.1;
 DR EMBL; U97142; AAC53300.1;
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 468 HYDROPHOBIC, REMOVED DURING MATURATION
 FT (POTENTIAL).
 FT DOMAIN 362 369 POLY-THR.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 347 347 POTENTIAL.
 FT CARBOHYD 406 406 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 SQ SEQUENCE 468 AA; 51649 MW; 6A7A2B2A CRC32;
 Query Match 23.3%; Score 511; DB 1; Length 468;
 Best Local Similarity 36.0%; Pred. No. 1.2e-34;
 Matches 130; Conservative 44; Mismatches 135; Indels 52; Gaps 13;
 QY 17 LMLLLPSPPLAAGDPLPTESRLMNSCLARRCQADPTCSAAYHLDSTS---- 70

Db 6 LYFALPLDLLLMSAEVSGDRL-----DCVKASDQCLKEGSCSTKRTLRRCVAGKE 57
 Oy 70 ---SISTPLPSEEPSPVADCLPAQAOLRNSSLIGCKCHRRKNQVACLDIYTVHARS 126
 Db 58 TWFSLTSLGLEAND-----ECRSAMEALKOKSLYNCRCKRGMKEKNCCLTIYWSMOSLO 112
 Oy 127 GNYELDVSPYEDVTYSKRPWKMLSKLNLKP-DSDL-----CLKFAMLCGLND 173
 Db 112 GNDLLEDSPEYE-----PVNSRLSDIFRAVPISDPVQOVEHISKGNCLDAKACNLD 165
 Oy 174 KCDRLRKAYGAGC-----SGPHQRHVCLROLITFEKKAEPHAGLLCPAPNDRCGE 229
 Db 166 TCKKRSAYITPCTTSMSEVNCNRKCKHAKLROFDDKVPKHSYGLMFCSC--RDIACTE 223
 Oy 230 RRRNTIAPNCALPP-VAPNCLTELRLCFSDPLCRSLVDVOTHCPRMD-ILGTCAEQ-S 286
 Db 224 RRQOTIVPVCSEYEEERENCLSLDSCRTNYICRSRLADFTTNCQPEBSKSYNCLKENYA 283
 Oy 287 RCLRAYLGLIGTAMTPNPNVSNVTVALSCTCRSGSNLOECCMLEGFFSHNPCLTIA 346
 Db 284 DCLAYISGLIGTAMTPNPNVSNVTVALSCTCRSGSNLOECCMLEGFFSHNPCLTIA 343
 Oy 347 A 347
 Db 344 A 344

RESULT 7

ID GDNF_HUMAN STANDARD: PRT: 464 AA.

AC P56159;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-ALPHA) (IGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1).
 GN GERAL OR GDNFRA OR TRNRI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SUBSTANTIA NIGRA;
 RX JING S., WEN D., YU Y., HOLST P.L., LUD Y., FANG M., TAMIR R., ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTRICK B.W., FOX G.M.;
 RA "GDNF-induced activation of the ret protein tyrosine kinase is mediated by GDNF-alpha, a novel receptor for GDNF";
 RL Cell 85:1113-1124(1996).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
 DR MIM: 601496;
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 428
 FT PROPEP 429 464
 FT DOMAIN 361 368
 FT CARBOHYD 39 39
 FT CARBOHYD 346 346
 FT CARBOHYD 405 405
 FT LIPID 428 428
 FT SEQUENCE 464 AA: 51291 MW: 2083574 CRC32:

Query Match 23.1%; Score 505.5; DB 1; Length 464;
 Best Local Similarity 36.3%; Pred. No. 3.3e-34;
 Matches 131; Conservative 45; Mismatches 132; Indels 53; Gaps 14;

Oy 17 LILLIPSPPLPAA---GDPLPTESLMNSCLQARRCQADPTCSAYNHIDSCTS---70
 Db 6 LYFALPLDLLLMSAEVSGDRL-----DCVKASDQCLKEGSCSTKRTLRRCVAGKE 57
 Oy 70 ---SISTPLPSEEPSPVADCLPAQAOLRNSSLIGCKCHRRKNQVACLDIYTVHARS 126
 Db 58 TWFSLTSLGLEAND-----ECRSAMEALKOKSLYNCRCKRGMKEKNCCLTIYWSMOSLO 112
 Oy 127 GNYELDVSPYEDVTYSKRPWKMLSKLNLKP-DSDL-----CLKFAMLCGLND 173
 Db 112 GNDLLEDSPEYE-----PVNSRLSDIFRAVPISDPVQOVEHISKGNCLDAKACNLD 165
 Oy 174 KCDRLRKAYGAGC-----SGPHQRHVCLROLITFEKKAEPHAGLLCPAPNDRCGE 229
 Db 166 TCKKRSAYITPCTTSMSEVNCNRKCKHAKLROFDDKVPKHSYGLMFCSC--RDIACTE 223
 Oy 230 RRRNTIAPNCALPP-VAPNCLTELRLCFSDPLCRSLVDVOTHCPRMD-ILGTCAEQ-S 286
 Db 224 RRQOTIVPVCSEYEEERENCLSLDSCRTNYICRSRLADFTTNCQPEBSKSYNCLKENYA 283
 Oy 287 RCLRAYLGLIGTAMTPNPNVSNVTVALSCTCRSGSNLOECCMLEGFFSHNPCLTIA 346
 Db 283 DCLAYISGLIGTAMTPNPNVSNVTVALSCTCRSGSNLOECCMLEGFFSHNPCLTIA 342
 Oy 347 A 347
 Db 343 A 343

RESULT 8

ID NOTC_DROME STANDARD: PRT: 2703 AA.

AC P07207; P04154;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR.
 GN N.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 86079939.
 RA WHARON K.A., JOHANSEN K.M., XU T., ARTAVANIS-TSAKONAS S.;
 RT "Nucleotide sequence from the neurogenic locus notch implies a gene product that shares homology with proteins containing EGF-like repeats";
 RT Cell 43:567-581(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OREGON-R;
 RX MEDLINE: 87064624.
 RA KIDD S., KELLEY M.R., YOUNG M.W.;
 RT "Sequence of the notch locus of Drosophila melanogaster: relationship of the encoded protein to mammalian clotting and growth factors";
 RL Mol. Cell. Biol. 6:3094-3108(1986).
 RN [3]
 RP SEQUENCE OF 2505-2611 FROM N.A.
 RX MEDLINE: 85099329.
 RA WHARON K.A., YEDOVONICK B., FINNERTY V.G., ARTAVANIS-TSAKONAS S.;
 RT "opa: a novel family of transcribed repeats shared by the Notch locus and other developmentally regulated loci in D. melanogaster";
 RL Cell 40:55-62(1985).
 RN [4]
 RP SEQUENCE OF 1-8 FROM N.A.
 RX MEDLINE: 87257846.

FT	DOMAIN	602	637	EGF-LIKE 15,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	639	677	EGF-LIKE 16,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	677	713	EGF-LIKE 17,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	715	751	EGF-LIKE 18,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	753	789	EGF-LIKE 19,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	791	827	EGF-LIKE 20,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	829	865	EGF-LIKE 21,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	867	905	EGF-LIKE 22,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	907	944	EGF-LIKE 23,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	946	982	EGF-LIKE 24,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	984	1020	EGF-LIKE 25,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1022	1058	EGF-LIKE 26,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1060	1096	EGF-LIKE 27,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1098	1134	EGF-LIKE 28,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1136	1181	EGF-LIKE 29,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1183	1219	EGF-LIKE 30,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1221	1257	EGF-LIKE 31,	CALCIUM-BINDING (POTENTIAL)
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FT	DOMAIN	1297	1335	EGF-LIKE 33,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1337	1373	EGF-LIKE 34,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1375	1412	EGF-LIKE 35,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1415	1451	EGF-LIKE 36,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1475	1593	3 x LIN/NOTCH REPEATS,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1475	1513	LIN/NOTCH 1,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1514	1553	LIN/NOTCH 2,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1554	1593	LIN/NOTCH 3,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1896	2109	6 x ANK MOTIF REPEATS,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	2538	2568	POLY-GLN (OPR-REPEAT),	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	62	73	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	67	83	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	85	94	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	100	111	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	105	124	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	126	135	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	143	154	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	148	164	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	166	175	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	181	192	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	186	203	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	205	214	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	221	232	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	226	241	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	243	252	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	259	270	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	264	279	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	281	290	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	292	308	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	302	317	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	319	328	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	335	349	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	343	358	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	360	369	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	376	387	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	381	396	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	398	407	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	413	424	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	418	435	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	437	446	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	453	465	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	459	474	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	476	485	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	492	503	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	497	512	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	514	523	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
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FT	DISULFID	552	561	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	568	579	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT					

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OM protein - protein search, using SW model

Run on: December 12, 1999, 20:17:02 ; Search time 27.76 Seconds
(without alignments)
626.999 Million cell updates/sec

Title: US-09-272-835-17

Sequence: 1 MWRPLNRPPLPVVLMILL.....FWVPSLFSCTPLILLSLW 369

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database:

PIR-62:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1458	72.1	397	2	JE0082	GPI-linked recepto
2	147.5	7.3	2703	1	A24420	notch protein - fr
3	126	6.2	3002	2	A47221	fibritin I precu
4	126	6.2	2871	2	A55567	fibritin I - bovl
5	124	6.1	2704	2	S09118	G-surface protein
6	123	6.1	3084	1	MMMSA	laminin alpha-1 ch
7	122.5	6.1	2321	2	S78349	notch3 protein - h
8	122.5	6.1	1964	2	T09059	notch4 - mouse
9	121	6.0	2555	2	A40043	notch protein homo
10	117.5	5.8	2718	2	A23475	G surface protein
11	117	5.8	384	2	S25771	gas1 protein - mou
12	115.5	5.7	2531	2	A49128	cell-fate determin
13	114.5	5.7	2531	2	A46019	Notch-1 protein - f
14	114.5	5.7	2139	2	A35672	crumbs protein - f
15	113.5	5.6	1034	2	JC5598	agrin - rat
16	112.5	5.6	1959	1	AGRT	laminin gamma-1 ch
17	111.5	5.5	1639	2	AS4105	fibritin-2 precu
18	111.5	5.5	2918	2	MMFBR2	tenascin precursor
19	111	5.5	2019	1	JQ1322	granulin precursor
20	110.5	5.5	553	1	GYHU	laminin alpha 5 ch
21	110.5	5.5	3635	2	T10053	laminin gamma-1 ch
22	110	5.4	1609	1	MMHUB2	fibritin-2 precu
23	110	5.4	2907	2	AS7278	laminin alpha-1 ch
24	109	5.4	4545	1	S25111	fibritin-2 precu
25	109	5.4	1203	2	A49117	fibritin-1 precu
26	107.5	5.3	2437	2	AS5624	transmembrane prot
27	107.5	5.3	2318	2	S42612	notch 3 protein -
28	107.5	5.3	2437	2	S45306	probable vitelloge
29	107	5.3	1984	2	T13171	Balbiani ring 3 pr
30	106.5	5.3	1700	2	S08167	fibulin 1 precursor
31	106.5	5.3	601	2	B36346	fibulin 1 precursor
32	106.5	5.3	683	2	C36346	apolipoprotein E r
33	106	5.2	996	2	JEO237	notch protein homo
34	106	5.2	2531	2	S18188	alpha-2-macroglobu
35	105.5	5.2	4544	1	S02392	laminin beta-1 cha
36	105.5	5.2	1766	1	MMMSB1	laminin gamma-1 ch
37	105.5	5.2	1607	1	MMMSB2	gas1 homolog - hum
38	105.5	5.2	345	2	AS5138	hypothetical prote
39	105.5	5.2	417	2	T08724	

40 105.5 5.2 473 2 A56175 adhesive plaque pr
41 104.5 5.2 593 2 S45281 coagulation factor
42 103.5 5.1 1296 2 T16859 hypothetical prote
43 103 5.1 4543 1 A53102 alpha-2-macroglobu
44 102.5 5.1 1810 1 A32230 tenascin precursor
45 102.5 5.1 1220 2 A56136 jagged protein pre

ALIGNMENTS

```

RESULT 1
JE0082
GPI-linked receptor precursor - mouse
N/Alternate names: GFalpha-3
C/Species: Mus musculus (house mouse)
C/Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 17-Mar-1999
C/Accession: JE0082
R/Nomoto, S.; Ito, S.; Yang, L.X.; Kiyuchi, K.
Biochem. Biophys. Res. Commun. 244, 849-853, 1998
A/Title: Molecular cloning and expression analysis of GFalpha-3, a novel CDNA related
A/Reference number: JE0082; MUID:98205811
A/Accession: JE0082
A/Molecule type: mRNA
A/Residues: 1-397 <NOM>
A/Cross-references: DDBJ:AB008833; NID:92627159; PID:92627160
C/Comment: This protein plays a distinct role in cell survival and differentiation.
C/Keywords: glycoprotein
F/1-25/Domain: signal sequence #status predicted <SIG>
F/380-397/Region: hydrophobic
F/92,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.1%; Score 1458; DB 2; Length 397;
Best Local Similarity 70.2%; Pred. No. 5.7e-108;
Matches 275; Conservative 29; Mismatches 56; Indels 32; Gaps 2;

QY 9 PLRPVLMILLPLPSPPLAAGDPLTESRLNMSCLOARRKCOADPTCSAAVHHLDSCT 68
D 1 PPRP-LIMLILVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACAAVQHLGSC 65
QY 69 SSISTPLPSEPSVPADCLAAOQLRNSSLGCGCHRRKNOVACLDITVTPARSL-- 127
D 66 SLSRPPLPESASACCLLEAEQLRNSSLIDCRRMRHOATCIDITVTPARSLGD 125
QY 127 -----SDSLCKRPMCTINDKCDRLRKAYGEGCSG 157
D 126 YELDVSPYEDTVISKPMKMLSKIMLKPSPDCLKRAMICTLHDKCDRLKAYGEGCSG 185
QY 158 PHCRHYCLQLLTFEKKAEPRHAGILLCPAPNDRCGERRRNTIAPNCALPPVAPNC 217
D 186 IRCRHCLQLSLTFEKKAEPRHAGILLCPAPNDRCGERRRNTIAPNCALPPVAPNC 245
QY 218 LELRFLFSPDLRSRHYDQTHCHPMDDIGTCAEDSRSLRAYLGLIGTAMPVNSV 277
D 246 LDLSFSPADPLCRSLRMDQTHCHPMDDIGTCAEDSRSLRAYLGLIGTAMPVNSISK 305
QY 278 NTVALSCRCRGSNGLOECCMELEGFSSHNPCLTEAIAAKMRHSOLFSDQMDHPFAV 337
D 306 NTVALSCRCRGSNGLOECCMELEGFSSHNPCLTEAIAAKMRHSOLFSDQMDHPFAV 365
QY 338 AHQENPAPVPPQVPSLFSCTPLILLSLW 369
D 366 QQONSMPALRLQPLRLPLSLPSILPLLILQLTW 397

RESULT 2
A24420
notch protein - fruit fly (Drosophila melanogaster)
N/Alternate names: neurogenic repetitive locus protein
C/Species: Drosophila melanogaster
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: A24420; A24768; S09358; A05267

```

R:Kidd, S.; Kelley, M.R.; Young, M.W.
 Mol. Cell. Biol. 6, 3094-3108, 1986
 A:Reference number: A24420; MUID:87064624
 A:Accession: A24420
 A:Molecule type: DNA
 A:Residues: 1-2703 <KID>
 A:Cross-references: GB:R03508; NID:q157991; PINN:AAA28725.1; PID:q157993
 R:Maron, K.A.; Johansen, K.M.; Xu, T.; Artaanis-Tsakonas, S.
 Cell 43, 567-581, 1985
 A:Reference number: A24768; MUID:86079539
 A:Accession: A24768
 A:Molecule type: mRNA
 A:Residues: 1-48, '1', 50-118, 'R', 120-230, 'T', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958,
 R:Rautz, D.
 Nucleic Acids Res. 17, 6463-6471, 1989
 A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA ma
 A:Reference number: S09358; MUID:89385974
 A:Accession: S09358
 A:Molecule type: DNA
 A:Residues: 2505-2551, 'QQQ', 2552-2576, 'E', 2578-2604 <TAU>
 R:Maron, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artaanis-Tsakonas, S.
 Cell 40, 55-62, 1985
 A:Title: opa: a novel family of transcribed repeats shared by the Notch locus and other
 A:Reference number: A05267; MUID:85093329
 A:Accession: A05267
 A:Molecule type: DNA
 A:Residues: 2504-2576, 'E', 2578-2611 <WHA2>
 A:Genetics:
 A:Gene: notch; opa
 A:Cross-references: FlyBase:FBgn0004647
 A:Map position: 8 96-9.36
 A:Residues: 53/3; 84/3; 171/3; 240/3; 283/3; 233/3; 2436/3; 2588/3
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C:Keywords: differentiation; tandem repeat; transmembrane protein
 F:27-43/Domain: transmembrane #status predicted <TM1>
 F:297-328/Domain: EGF homology <EGF1>
 F:530-561/Domain: EGF homology <EGF2>
 F:568-599/Domain: EGF homology <EGF>
 F:988-1018/Domain: EGF homology <EGF2>
 F:1064-1095/Domain: EGF homology <EGF3>
 F:1187-1218/Domain: EGF homology <EGF3>
 F:1746-1762/Domain: transmembrane #status predicted <TM2>
 F:1950-1982/Domain: ankyrin repeat homology <AN1>
 F:1983-2015/Domain: ankyrin repeat homology <AN2>
 F:1988-2004/Domain: transmembrane #status predicted <TM3>
 F:2012-2049/Domain: ankyrin repeat homology <AN3>
 F:2050-2082/Domain: ankyrin repeat homology <AN4>
 F:2083-2115/Domain: ankyrin repeat homology <AN5>
 F:238-2568/Region: glutamine-rich
 F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 7.3%; Score 147.5; DB 1; Length 2703;
 Best Local Similarity 20.9%; Pred. No. 0.001;
 Matches 82; Conservative 37; Mismatches 120; Indels 153; Gaps 22;

QY 41 MNSCLARRKQADPTCSAYHLDSCSTSTPTL-----PSEPEVPADCLEAAQ 92
 DB 985 INECIS--OPCNGATCS--QVNSYCT-----CPIGFSGINGQTNDEDTESCLNGGSC 1037
 QY 93 L-----NNSLIGCMCR----- 106
 DB 1038 IINGINGNCISLAGYSGANCQYKLNKCDNPNCLNGATCHEONNEYTCHEPSTGTCQCE 1097
 QY 106 -----RAKNQVAC-LDYVTWTHARASLDSLC-----L 132
 DB 1098 YDWMGQSPCEGATCSQKHKHPSCKSGSGWT-----GKLCVQYITSCDADADRGL 1149
 QY 133 KRAMCLTLNKKCDRLKAYGEA-----CS-----GPHCORHV-----CLRLQLTF 172
 DB 1150 SLROLGN-NGTC-----KDYGNHVCYCSGSGYAGSYCQKREIDSCQSGPQONGSTCHDLIGA 1204

QY 173 FEKRAEPHAG-----LLPCCAPN--DRG--CGERRNTIAPNCALPVAPNCL-ELRR- 223
 DB 1205 YEQCGQGRFGQNCNELINDIDCAPNPQNGNGTCHDRMNF---SCSPPTMTGICINKD 1261
 QY 223 -----LCFSDPLCRSLVDVQTHCHPMIDILGTCAREQSRCLRAYIGLTAMTPNEVSNV 277
 DB 1262 DCRPGACHNNGSCIDVVGFEVCQPGFVGARCEGIDNCLSPNSMAGTLDCVQLVNNY 1321
 QY 278 NTSVALSCTRGSGNQLCECEMLEGFEFSNHC 309
 DB 1322 H-----CNCR-PGHMGRHCEHKVDFCAQSPC 1346

RESULT 3
 A47221
 fibrillin 1 precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999
 C:Accession: A47221; 154355; S17064; 159574; S17062; S6211; A34198
 R:Corson, G.M.; Chabberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.
 Genomics 17, 476-484, 1993
 A:Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain stru
 A:Reference number: A47221; MUID:94010947
 A:Accession: A47221
 A:Molecule type: mRNA
 A:Residues: 1-337, 'T', 339-1029 <COR>
 A:Cross-references: GB:X63556
 R:Perleir, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangillan, T.; Bo
 Hum. Mol. Genet. 2, 961-968, 1993
 A:Title: Genomic organization of the sequence coding for fibrillin, the defective gen
 A:Reference number: 154355; MUID:93372860
 A:Accession: 154355
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 132-3002 <PER>
 A:Cross-references: GB:LI3923; NID:9306745; PID:9306746
 R:Maehlen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.
 Nature 352, 334-337, 1991
 A:Title: Partial sequence of a candidate gene for the Marfan syndrome.
 A:Reference number: S17064; MUID:91304568
 A:Accession: S17064
 A:Molecule type: mRNA
 A:Residues: 1030-3002 <NAS>
 A:Cross-references: EMBL:X63556
 R:Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.
 Science 259, 680-683, 1993
 A:Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
 A:Reference number: 159574; MUID:93157831
 A:Accession: 159574
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 2217-2288, 'T', 2290-2325 <RES>
 A:Cross-references: GB:S54426; NID:9264860; PID:9264861
 R:Lee, B.; Godfrey, M.; Vitale, E.; Horl, H.; Mattel, M.G.; Sarfarazi, M.; Tsipouras,
 Nature 352, 330-334, 1991
 A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two diff
 A:Reference number: S17062; MUID:91304567
 A:Accession: S17062
 A:Molecule type: mRNA
 A:Residues: 'VAVTVFIFLSYKML', 944-1444 <LEE1>
 A:Cross-references: EMBL:X62008
 A:Accession: S62111
 A:Molecule type: Protein
 A:Residues: 1166-1176, 'Y', 1178-1180, 'D', 1182-1185 <LEE2>
 R:Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
 J. Biol. Chem. 264, 21381-21385, 1989
 A:Title: Connective tissue microfibrils. Isolation and characterization of three larg
 A:Reference number: A34198; MUID:90078246
 A:Accession: A34198
 A:Molecule type: Protein
 A:Residues: 565-575, 1890-1892, 'T', 1894-1900 <MAD>
 C:Comment: Fibrillin is a major component of elastin-associated microfibrils.
 C:Genetics:

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:45:08 ; Search time 20.22 Seconds
(without alignments)
530.797 Million cell updates/sec

Title: US-09-272-835-17
Perfect score: 2022
Sequence: 1 MVRNLRNPRLPPVYLMILL.....PMVSLFECTPLILLISLW 369

Scoring table: BLOSUM62

Searched: 80000 seqs, 29085965 residues

Database: SWISSPROT_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	538.5	26.6	465	1 NRTN_CHICK	013157 gallus gall
2	513	25.4	463	1 NRTN_MOUSE	008842 mus musculu
3	509	25.2	464	1 NRTN_HUMAN	000451 homo sapien
4	503	24.9	469	1 GDNF_CHICK	013156 gallus gall
5	485.5	24.0	468	1 GDNF_MOUSE	097785 mus musculu
6	483.5	23.9	468	1 GDNF_RAT	062997 rattus norv
7	475	23.5	464	1 GDNF_HUMAN	056159 homo sapien
8	475	23.5	464	1 GDNF_MOUSE	070707 dtrosophila
9	126	6.2	2871	1 FBNI_BOVIN	098133 bos taurus
10	126	6.2	2871	1 FBNI_HUMAN	035555 homo sapien
11	124	6.1	2704	1 G168_PARP	017053 paramescium
12	123	6.1	3084	1 LMAL_MOUSE	019137 mus musculu
13	122.5	6.1	1964	1 NTC4_MOUSE	031695 mus musculu
14	121	6.0	2444	1 NTC4_HUMAN	046531 homo sapien
15	117.5	5.8	2715	1 G156_PARP	013837 paramescium
16	117	5.8	384	1 CAS1_MOUSE	001721 mus musculu
17	114.5	5.7	2139	1 CRB_DROME	010040 dtrosophila
18	114.5	5.7	2531	1 NTC1_MOUSE	001705 mus musculu
19	112.5	5.6	1959	1 AGRI_RAT	023304 rattus norv
20	111.5	5.5	2911	1 FBNI_HUMAN	035555 homo sapien
21	110.5	5.5	593	1 GRN_HUMAN	028799 homo sapien
22	110.5	5.5	3635	1 LMAS_MOUSE	061001 mus musculu
23	110	5.4	2907	1 FBNI_MOUSE	061555 mus musculu
24	110	5.4	1609	1 LMGI_HUMAN	061554 mus musculu
25	109	5.4	2871	1 FBNI_MOUSE	061554 mus musculu
26	107.5	5.3	1639	1 LMGI_DROME	015215 dtrosophila
27	107.5	5.3	2437	1 NTC3_MOUSE	061554 mus musculu
28	107.5	5.3	2318	1 NTC3_MOUSE	061554 mus musculu
29	107	5.3	1984	1 YL_DROME	061554 mus musculu
30	106.5	5.3	1700	1 BAR3_CHITE	003376 chironomus
31	106.5	5.3	566	1 FBIL_HUMAN	023142 homo sapien
32	106.5	5.3	601	1 FBIL_HUMAN	023142 homo sapien
33	106.5	5.3	683	1 FBIL_HUMAN	023142 homo sapien
34	106.5	5.3	703	1 FBIL_HUMAN	023142 homo sapien
35	106	5.2	4660	1 LRP2_RAT	023142 homo sapien
36	106	5.2	2531	1 NTC1_RAT	007008 rattus norv
37	105.5	5.2	345	1 CAS1_HUMAN	034826 homo sapien
38	105.5	5.2	1767	1 LMGI_MOUSE	02468 mus musculu
39	105.5	5.2	1607	1 LMGI_MOUSE	02468 mus musculu
40	105.5	5.2	4544	1 LRP1_HUMAN	007954 mus sapien
41	104.5	5.2	593	1 FBIL_BOVIN	098140 bos taurus
42	103	5.1	4543	1 LRP1_CHICK	098157 gallus gall
43	102.5	5.1	3672	1 LML2_CAEEL	021313 caenorhabd1

ALIGNMENTS

RESULT	1	STANDARD	PRT	465 AA
NRTN_CHICK				
1 NRTN_CHICK				
AC 013157				
DT 01-NOV-1997 (Rel. 35, Created)				
DT 01-NOV-1997 (Rel. 35, Last sequence update)				
DT 15-DEC-1998 (Rel. 37, Last annotation update)				
DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NRTN-ALPHA) (NRTN-ALPHA) (GDNF				
DE RECEPTOR BETA) (GDNF-BETA).				
GN GFR2 OR GDNFB.				
OS Gallus gallus (Chicken).				
OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;				
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				
11				
RP SEQUENCE FROM N.A.				
RC TISSUE-BRAIN:				
RX MEDLINE: 9736104.				
RA BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,				
RA ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.,				
RT "Neurturin responsiveness requires a GPI-linked receptor and the Ret				
RT receptor tyrosine kinase."				
RL Nature 387:721-724(1997).				
CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED				
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE				
CC TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE				
CC RECEPTOR (BY SIMILARITY).				
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.				
CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.				
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CC or send an email to license@sb-sib.ch).				
CC				
DR EMBL: U90542; AB061571.1; -				
KM Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.				
FT SIGNAL	1	21		
FT CHAIN	22	445		
FT PROPEP	446	465		
FT				
FT CARBOHYD	355	355		
FT CARBOHYD	387	387		
FT CARBOHYD	412	412		
FT LIPID	445	445		
FT SEQUENCE	465 AA;	51908 MW;	5CA073EA	CRC32;
Query Match	26.6%	Score 538.5;	DB 1;	Length 465;
Best Local Similarity	33.4%	Pred. No. 2e-37;		
Matches 127;	Conservative 46;	Mismatches 138;	Indels 69;	Gaps 11;
OY 19 LILPPSPPLAAGPLPTESS---RLMNSCLQARRKQADPTGSAAYHHIDSGTS--SIS 72				
DB 20 LADPSP-----PGQDQGNRPVVDICIRANKLCAAGSCSSSRRTLRQCIAGDRN 70				
OY 73 TPLPSEPSPADCLAAQOLRNSLIGCMCHRRKNOVACLIYTVH-----122				
DB 71 TMLANK-----QQALETVLOESPPLYDCCKGKRMKEICLOVYTSIHGLAGEGEPTE 124				
OY 122 -----PARSLSDSLCLFAMLCITLNDKCDRLKRAYGACS 156				
DB 125 ASPEYPTSLRSLDFILASIFSGMDPATNSKSHNCLDAACACILNDNCKRLRGISTOS 184				

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OY 157 -----GPHCRHVCLRLTFFEKAAEPHAGOLLCPCAPNDROGGERRTIAPNCAL- 211
DB 165 KEISATHECSRRKCHKALROFFDNPVSEYTRLLFCSC--KDOACAEPRRQTIYPCFSYE 242
OY 211 PPAVNCLELRRLCFSDPCLSRVDFOTCH-PMIDIGTCATEO-SRECLRAYGLIGTA 268
DB 243 DKRPNCLDLRNVCADHLCRSRLADFHANQASFOGLTSCPGNYOAGLSYGLIGFD 302
OY 269 MTPNPNVSVNTSVALS--CTCRGSGNLOEECEEMLEGGFSSNPPCLTEAIANMRHSQLFS 326
DB 303 MTPNPNVASTSTISIPWCSCKSGNLEECCEKRLROFTENPCLRNIAIOAFNGTGVNLS 362
OY 327 QDMHPTFAVMAHONENPAV 346
DB 363 PKNPSPTMLPKYKSPAL 382

RESULT 2
NRTN_MOUSE STANDARD; PRT; 463 AA.
008842:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
DE (GDNF-BETA)
GN GFRA2 OR GDNFRB OR TRNR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97325791.
RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
RA HEUCKEROFF R.O., KECK C.L., ZIMONJIC D.B., POPOSCU N.C.,
RA JOHNSON E.M. JR., MILBRANDT J.;
RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling
RT through Ret.";
RL Neuron 18:793-802(1997).
CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
CC TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CERVICAL AND DORSAL
CC ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEEN
CC AND IN THE ADRENAL.
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL, AF002701; AAC53548.1; -
CC DR MGD; MG1:1195462; GFRA2.
CC KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal;
CC Alternative splicing.
CC FT SIGNAL 1 21
CC FT CHAIN 22 443
CC FT PROPEP 444 463
CC FT CARBOHYD 52 52
CC FT CARBOHYD 357 357
CC FT CARBOHYD 413 413
CC FT LIPID 443 443
CC FT GPI-ANCHOR (POTENTIAL).

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FT VARSPIC 14 146 MISSING (IN SHORT FORM).
SQ SEQUENCE 463 AA; 51598 MW; 0A2165C0 CRC32;
Query Match 25.4%; Score 513; DB 1; Length 463;
Best Local Similarity 33.8%; Pred. No. 2,6e-35;
Matches 122; Conservative 42; Mismatches 131; Indels 66; Gaps 11;
OY 44 CLOARRKQADPTCSAAYHLDSCTS--SISTLPSESPVADPCLEAQQLRNSLIGC 101
DB 40 CVANELCALESNCSSRYRLRCLAGRDNRNTLANKE-----CQALEVLDSPLYDC 93
OY 102 MCHRRKNOVACLDITWYHAR----- 125
DB 94 RCRGRKKELQCIQIYWSIHILGTEGEFEYAEPEPYTSRLSDIFRLASIFSGTADPV 153
OY 125 -SLDSCLKFAMLCTLNKCDLRYAGEACS-----GPHCRHVCLRLTFFEKAAE 178
DB 154 VSAKSNHCLDPAACNLNCKRLRSSYISICNREISPTERCNRRCHKALROFFRVPS 213
OY 179 PHAAGLLCPCAPNDROGGERRTIAPNCAL-PPVAPNCLERRLCFSDPCLSRSLYDF 237
DB 214 EYIYRLFCSC--QDQACAEPRRQTIYPCFSYEDKPKCLDRSLCRTDHLCRSLADF 271
OY 238 QTRCHP--MDLIGTCATEOSRCLRAYGLIGTAMPEFVSNTSVALS--CTCRGSGNL 293
DB 272 HANCRASYRTITSCPADNTQACIGSYAGMIGDMFNYYDSNTGTIVSPKCRSGGN 331
OY 294 QEECEMLEEFPFHNPCLTALIAAKRHSQLSQDMH-PTAVMAHONENPAVRDQPV 352
DB 332 EEECEFLNDFENPCLRNAIOA--FGNGTDVNSPKGPTESA---TQAPVKEPTSL 384
OY 353 P 353
DB 385 P 385

RESULT 3
NRTN_HUMAN STANDARD; PRT; 464 AA.
000451:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
DE (GDNF-BETA)
GN GFRA2 OR GDNFRB OR TRNR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97325791.
RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
RA HEUCKEROFF R.O., KECK C.L., ZIMONJIC D.B., POPOSCU N.C.,
RA JOHNSON E.M. JR., MILBRANDT J.;
RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling
RT through Ret.";
RL Neuron 18:793-802(1997).
CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
CC TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
CC SPLICING IN BOTH BRAIN AND PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
CC -----
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 CC -----
 DR EMBL: AF002700; AAC52036.1; -
 DR MIM: 601956; -
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal;
 KW Alternative splicing.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 444 NEURITIN RECEPTOR ALPHA.
 FT PROPEP 445 464 HYDROPHOBIC, REMOVED DURING MATURATION
 FT CARBOHYD 52 52 (POTENTIAL).
 FT CARBOHYD 357 357 (POTENTIAL).
 FT CARBOHYD 413 413 POTENTIAL.
 FT LIPID 444 444 GPI-ANCHOR (POTENTIAL).
 FT VARPPLIC 14 14 MISSING (IN SHORT FORM).
 FT SEQUENCE 464 AA; 51558 MW; 3C74BBB CRC32;
 Query Match 25.2%; Score 509; DB 1; Length 464;
 Best Local Similarity 34.4%; Pred. No. 5.5e-35;
 Matches 111; Conservative 41; Mismatches 113; Indels 58; Gaps 8;
 QY 44 CQARRKCOADPTCSAAYHLDSCS--SISTPLPEEPSPADCLEAQAOLNSSLIGC 101
 DB 40 CVRAMELCAESCSRYTLRCLAGRDNTLANKE-----COALEVLOESPLYDC 93
 QY 102 MHRMRKNVACLDITYWYHRA----- 125
 DB 94 RCKRGKKELQCIQIYWSIHLGTEGEFEYEAAPYVTSRLSDIFRLASIFSGTGADPY 153
 QY 125 -SLDSDLCKFPMMLCTLNKCDRLKRAYGEAC-----GPHCRHICLROLTFEKKAE 178
 DB 154 VSAKSNHCLDAKACACNLNCKKRLSSYSICNREISPERCKRRCKHALRQFPDRVPS 213
 QY 179 PHAGILLPCAPANDRGCGERRNTIAPNCAL-PPVAPNCLRLRCLFSPDLGRSLYDF 237
 DB 214 EYTYMMLFQSC--QQAQACERRRQTLIPSCSYEDKPKNCLDRGVCRDHLCRSRLADP 271
 QY 238 QTHCHP--MDIGTCATEOSRCLRAYLIGTAMPNPNVSNVNTVALS--CTCRSGNLT 293
 DB 292 HANCRASYOTVTSADPNYQACIGSYAGMIGFDMPTNYDSSPTGLIVSPWCSGCRSGNM 331
 QY 294 OECEMELGEGFHSNPLCTEATAIA 316
 DB 332 EEECEFLDFEENPCLRNAIOA 354
 RESULT 4
 GDNF_CHICK STANDARD: PRT; 469 AA.
 ID GDNF_CHICK
 AC 013156;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
 DE NEUROTROPIC FACTOR RECEPTOR 1).
 DE GFRAL OR GDNFRA.
 OS Gallus gallus (Chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 OS Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RC MEDLINE; 97336104.
 RA BUY-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,
 RA ROSENTHAL A., CHINCHETRU M., BUCHANAN V.L., DAVIES A.M.;
 RA "Neuritin responsiveness requires a GPI-linked receptor and the Ret
 RA receptor tyrosine kinase".
 RA Nature 387:721-724(1997).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED

CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U90541; AAB61570.1; -
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
 KW SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 469 HYDROPHOBIC, REMOVED DURING MATURATION
 FT DOMAIN 361 368 POLY-THR.
 FT CARBOHYD 62 62 POTENTIAL.
 FT CARBOHYD 163 163 POTENTIAL.
 FT CARBOHYD 346 346 POTENTIAL.
 FT CARBOHYD 405 405 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 FT SEQUENCE 469 AA; 52043 MW; C8D241C9 CRC32;
 Query Match 24.9%; Score 503; DB 1; Length 469;
 Best Local Similarity 35.3%; Pred. No. 1.7e-34;
 Matches 123; Conservative 42; Mismatches 127; Indels 56; Gaps 11;
 QY 16 MLLLLPSPPLIAG-DPLPESRLMSCLDARRKCOADPTCSAAYHLDSCS----- 70
 DB 5 LYLIALPLADVLLSEVSGLPBGDRL--DCVVASDQCKECSYKRYTLRQCVAGKESN 62
 QY 70 -SISTPLPEEPSPADCLEAQAOLNSSLIGCMHRMKNVACLDITYWYHRA----- 124
 DB 63 FSRAGLEAKD-----ECKSAMKALKOKSLYNCRRKRGKKKCKLRITYWSYOSLGND 117
 QY 124 -----RSLSDL-----CLFAMLCITLDCDRLKRAYGEAC 155
 DB 118 LLEDSPYEPVNSRLSDIFRLAIVSEVPLSGNNGCLDAARACNLNDCKFRSAIYTPC 177
 QY 156 -----SGPHCQHVCLRLQTLTFEKAEPHAGLLICPCAPNDRGCGERRNTIAPNCALP 211
 DB 178 TSTSTNEICNKKRCKALRLEFDKVPKHSYGMLEFCSC--RDVACTERRROTIVPVCSYE 235
 QY 212 P-VAPNCLRLRCLGSDPLCRSLYDPOTHCPMD-IIGTCATED-SICLAYLGLIGTA 268
 DB 236 DREKNCNLDSCKKNTICSRLLDFTNCPESRSVSSCLKEKYACCLLAYSGLTGTV 295
 QY 269 MTPNFVSNVNTVALSCTCRSGNLOECEMELGEGFHSNPLCTEATAIA 316
 DB 296 MTPNTDSSLSVAPWCMGCSNGNDIDECRFNFQDNTCLXNAIOA 343
 RESULT 5
 GDNF_MOUSE STANDARD: PRT; 468 AA.
 ID GDNF_MOUSE
 AC P97785;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
 DE NEUROTROPIC FACTOR RECEPTOR 1).
 DE GFRAL OR GDNFRA OR TRNRL.
 OS Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-DORSAL ROOT GANGLION;
 RA MATABE K.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AB000800; BAI19185.1;
 DR MGD; MG11100842; GFR1.
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; signal.
 FT SIGNAL 1 24
 FT CHAIN 25 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 468 HYDROPHOBIC, REMOVED DURING MATURATION
 FT (POTENTIAL).
 FT DOMAIN 362 369 THR-RICH.
 FT CARBOHYD 359 359 POTENTIAL.
 FT CARBOHYD 347 347 POTENTIAL.
 FT CARBOHYD 406 406 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 SO SEQUENCE 468 AA; 51782 MW; 6C64C182 CRC32;

Query Match 24.0%; Score 485.5; DB 1; Length 468;
 Best Local Similarity 34.3%; Pred. No. 4.8e-33;
 Matches 121; Conservative 42; Mismatches 123; Indels 67; Gaps 11;

QY 14 VMLLLPSPPLAAGDPLPESRLMNSCLARRKQADPCSAAYHHLDSCTS---70
 DB 9 VLPLDLMLNSA-EVSGDRL-----DCVRAADQCLKEGSCSKYRRLRQCVAGKEM 58
 QV 70 -SISPLPEEPSPADCLAAQOLRNSLLICMCHRRKNVACLDIYTH-----122
 59 NESTLSTGLKAD-----ECNSAEALAKQSLYNCRCRGRKRNCLRTIYWSYQSLQGN 113
 QY 122 -----PARSLDSL-----CLKFAMLCTLNDKDLRKA 150
 DB 114 DLLEDSPEYEVNRLSDIFRAVPIISDYPOVHEHISKGNKNCDAARACHLDQCKRYRRA 173
 QY 151 YGAGAC-----SGPRQORHVCRLQLTFEFAAEPAEHAQGLLPCAPDRKCGERRRTIAP 206
 DB 174 YTPCTTSNSNEVCNRRKCKHKLROFFDKYPAKHSYGLMFCSC--RDVACTERRQITIP 231
 QY 207 NCALPP-VAPNCLERLRFESDPLCRSLVDPTQHPMD-ILGTATATQ-SKCLRAYTG 263
 DB 232 VCYEERERENCLNTDSCRTNTICRSLADEFTNCPQPSRSVSNCLKNYDCLLAYSG 291
 QY 264 LIGTATPPEVSNVNTVALSCTCRGSGNLQEECEMLLEFFSINPCLTAIAA 316
 DB 292 LIGTATPPEVSNVNTVALSCTCRGSGNLQEECEMLLEFFSINPCLTAIAA 344

RESULT 6
 GDNF_RAT
 ID GDNF_RAT STANDARD; PRT; 468 AA.
 AC 062397;
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-ALPHA) (TGF-BETA RELATED
 DE NEUROTROPHIC FACTOR RECEPTOR 1) (RET LIGAND 1).
 GN GFR1 OR GDNFRA OR TNRI OR RETL.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-RETINA;
 RX MEDLINE: 96270513.
 RA JING S., WEN D., YU Y., HOLST P.L., LUO Y., FANG M., TAMIR R.,
 RA ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTHROCK B.W.,
 RA FOX G.M.;
 RT "GDNF-induced activation of the ret protein tyrosine kinase is
 RT mediated by GDNF-alpha, a novel receptor for GDNF."
 RL Cell 85:1113-1124(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MISTAR; TISSUE-KIDNEY;
 RX MEDLINE: 97322356
 RA SANTOCLA M., HESSION C.A., WORLEY D.S., CARNILLO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 RT can be mediated by two different cell-surface accessory proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96273032.
 RA TREANOR J.J.S., GOOGMAN L., DE SAUVAGE F., STONE D.M., POULSEN K.T.,
 RA BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HEFT F.,
 RA PHILLIPS H.S., GODDARD A., MOORE M.W., BOUT-BELLO A., DAVIES A.M.,
 RA ASAI N., TAKAHASHI M., VANDLEN R., HENDERSON C.E., ROSENTHAL A.;
 RT "Characterization of a multicomponent receptor for GDNF."
 RL Nature 382:80-83(1996).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: U59486; AAC52663.1;
 DR EMBL: U97142; AAC53300.1;
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; signal.
 FT SIGNAL 1 24
 FT CHAIN 25 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 468 HYDROPHOBIC, REMOVED DURING MATURATION
 FT (POTENTIAL).
 FT DOMAIN 362 369 POLY-THR.
 FT CARBOHYD 359 359 POTENTIAL.
 FT CARBOHYD 347 347 POTENTIAL.
 FT CARBOHYD 406 406 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 SO SEQUENCE 468 AA; 51649 MW; 6A7A2B2A CRC32;

Query Match 23.9%; Score 483.5; DB 1; Length 468;
 Best Local Similarity 34.2%; Pred. No. 7.1e-33;
 Matches 121; Conservative 40; Mismatches 124; Indels 69; Gaps 11;

QY 17 LLLPLPSPPLAAGDPLPESRLMNSCLARRKQADPCSAAYHHLDSCTS---70

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Db 6 LYPALPDLILMSVSGDRL-----DCVKASDQCLKEQSCSTKRTYLRQCVAGKE 57
Qy 70 ----SISTPLPSEPSVPADCLEAAQOLRNSLLIGCMCHRRKNOVACLDIYVTHA----- 122
Db 58 TNSLSLGLAKD-----BERSAMEALKOKSLYNCRCRKKKCKKNCCLRIYWSYMSLOG 112
Qy 122 -----PARSLSDL-----CLNFAMLCITLNDKCDRLRK 149
Db 113 NDLEDSPEYEPVNSRLSDIFRAVYFISDFVQVEHISKGNNCIDAAKACNLDIDCKKYS 172
Qy 150 AYGEAC-----SGHCHQRHVCRLRLTFEKAEPHAGLLCPCAPNDGCGERRNTIA 205
Db 173 ATTPCTSYSDNVCNRRCKHKLROFFDKVPARKSHYGMJFCSC--RDIACTERRRQTIY 230
Qy 206 PNCALPP-VAPNCLLELRCLFSDPLCRSLVDFOHCHPMD-ILGTCAEQ-SRCLRAYL 262
Db 231 PVSYSEREPNCL-LQDSCKTYICRSRLADFTTNCOPESRSVSCLENTYADCLAYS 290
Qy 263 GLIGTAMPTNVSNTSVYALSCTCRSGNLOECEMLEGFFSHNPLCTEATIA 316
Db 291 GLIGTAMPTNYSIDSSLSVAPMCDGNSGNDLECLKLFNFNDNTCLNAIQA 344

RESULT 7
GDNF_HUMAN
ID GDNF_HUMAN STANDARD; PRT; 464 AA.
AC P56159;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
DE NEUROTROPHIC FACTOR RECEPTOR 1).
GN GFRAL OR GDNFRA OR TRNRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP TISSUE-SUBSTANTIA NIGRA;
RX MEDLINE; 96270513.
RA JUNG S., WEN D., YU Y., HOUST P.L., LIO Y., FANG M., TAMIR R.,
RA ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTROCK B.W.,
RA FOX-G.M.;
RA "GDNF-induced activation of the ret protein tyrosine kinase is
RA mediated by GDNFR-alpha, a novel receptor for GDNF.";
RA Cell 85:1113-1124(1996).
RN [1]
RP FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
RP AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
RP SIMILARITY).
CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
CC WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
DR MIM: 601496;
KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 428 GDNF RECEPTOR ALPHA.
FT PROPEP 429 464 HYDROPHOBIC, REMOVED DURING MATURATION
FT (POTENTIAL).
FT DOMAIN 361 368 POLY-THR.
FT CARBOHYD 59 59 POTENTIAL.
FT CARBOHYD 346 346 POTENTIAL.
FT CARBOHYD 405 405 POTENTIAL.
FT LIPID 428 428 GPI-ANCHOR (POTENTIAL).
FT SEQUENCE 464 AA; 51291 MW; 2C8C3574 CRC32;
Query Match 23.5%; Score 475; DB 1; Length 464;
Best Local Similarity 34.2%; Pred. No. 3.5e-32;
Matches 121; Conservative 42; Mismatches 121; Indels 70; Gaps 12;

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Qy 17 LLLPLPSPPLPLA-----GDPPLTESLNMNSCLARRKQADPTCSAAHHLDSCS---- 70
Db 6 LYPALPDLILMSVSGDRL-----DCVKASDQCLKEQSCSTKRTYLRQCVAGKE 57
Qy 70 ----SISTPLPSEPSVPADCLEAAQOLRNSLLIGCMCHRRKNOVACLDIYVTHA----- 124
Db 58 TNSLSLGLAKD-----BERSAMEALKOKSLYNCRCRKKKCKKNCCLRIYWSYMSLOG 112
Qy 124 -----RSLSDL-----CLNFAMLCITLNDKCDRLRK 149
Db 113 NDLEDSPEYEPVNSRLSDIFRAVYFISDFVQVEHISKGNNCIDAAKACNLDIDCKKYS 172
Qy 150 AYGEAC-----SGHCHQRHVCRLRLTFEKAEPHAGLLCPCAPNDGCGERRNTIA 205
Db 173 ATTPCTSYSDNVCNRRCKHKLROFFDKVPARKSHYGMJFCSC--RDIACTERRRQTIY 230
Qy 206 PNCALPP-VAPNCLLELRCLFSDPLCRSLVDFOHCHPMD-ILGTCAEQ-SRCLRAYL 262
Db 231 PVSYSEREPNCL-LQDSCKTYICRSRLADFTTNCOPESRSVSCLENTYADCLAYS 289
Qy 263 GLIGTAMPTNVSNTSVYALSCTCRSGNLOECEMLEGFFSHNPLCTEATIA 316
Db 290 GLIGTAMPTNYSIDSSLSVAPMCDGNSGNDLECLKLFNFNDNTCLNAIQA 343

RESULT 8
NOTCH_DROME
ID NOTCH_DROME STANDARD; PRT; 2703 AA.
AC P07207; P04154;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR.
GN N.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86079539.
RA WHARTON K.A., JOHANSEN K.M., XU T., ARTAVANIS-TSAKONAS S.;
RA "Nucleotide sequence from the neurogenic locus notch implies a gene
RA product that shares homology with proteins containing EGF-like
RA repeats.";
RA Cell 43:567-581(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-OREGON R;
RX MEDLINE; 87064624.
RA KIDDO S., KELLEY M.R., YOUNG M.W.;
RA "Sequence of the notch locus of Drosophila melanogaster: relationship
RA of the encoded protein to mammalian clotting and growth factors.";
RA Mol. Cell. Biol. 6:3094-3108(1986).
RN [3]
RP SEQUENCE OF 2505-2611 FROM N.A.
RX MEDLINE; 85099329.
RA WHARTON K.A., YEDVOBNICK B., FINNERTY V.G., ARTAVANIS-TSAKONAS S.;
RA "opa: a novel family of transcribed repeats shared by the Notch locus
RA and other developmentally regulated loci in D. melanogaster.";
RA Cell 40:55-62(1985).
RN [4]
RP SEQUENCE OF 1-8 FROM N.A.
RX MEDLINE; 87257846.
RA KELLEY M.R., KIDDO S., BERG R.L., YOUNG M.W.;
RA "Restriction of P-element insertions at the Notch locus of Drosophila
RA melanogaster.";
RA Mol. Cell. Biol. 7:1545-1548(1987).
RN [5]
RP REVIEW.
RA HARRIS W.A.;
RA "Many cell types specified by Notch function.";

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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:20:30 ; Search time 33.26 Seconds

(without alignments)
1635.437 Million cell updates/sec

Title: us-09-272-835-20

Sequence: 1 MGSTAAAGLAVILFVIVGL.....DASLRKADPNFRCKDLPVL 888

Scoring table: BLOSUM62

Searched: 199794 seqs, 61255205 residues

Database:

SPTREMBL.11.*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2400	51.3	884	4	014953
2	2337.5	50.0	723	4	012787
3	2246	48.0	876	11	060752
4	2080	44.5	866	11	062121
5	1888	40.4	397	11	055243
6	1888	40.4	397	11	035325
7	1880	40.2	397	11	035118
8	1728.5	37.0	873	13	098949
9	1564	33.5	400	4	060609
10	1287	27.7	874	13	097166
11	1155.5	24.7	999	4	012866
12	1146	24.5	511	11	062194
13	1137	24.3	994	11	060805
14	1102.5	23.6	974	13	090777
15	811	17.3	600	4	015516
16	697	14.9	1369	13	P79950
17	686	14.5	1369	13	P70003
18	678	14.5	1374	13	P70003
19	668.5	14.3	570	5	097191
20	662.5	14.2	596	12	085458
21	659.5	14.1	1375	13	09YGM5
22	658.5	14.1	1404	13	008757
23	645.5	13.8	1378	11	062190
24	645.5	13.8	1382	11	062555
25	617.5	13.2	1425	13	09YGM7
26	615	13.0	1382	11	P97579
27	609	12.9	455	4	012875
28	605	12.9	2554	5	024512
29	602	12.9	2554	5	024512

30	600	12.8	1373	11	070438
31	597	12.8	1382	11	P97523
32	588.5	12.6	609	13	091776
33	586	12.5	464	11	035977
34	585	12.5	464	11	035962
35	582.5	12.5	1418	13	093457
36	582	12.4	464	4	015316
37	582	12.4	464	4	015328
38	579.5	12.4	1358	13	073798
39	579.5	12.4	1064	13	090601
40	578.5	12.4	1106	13	P79726
41	577	12.3	1106	13	042362
42	574	12.3	476	13	073845
43	570.5	12.2	981	12	039477
44	570.5	12.2	980	12	092809
45	570.5	12.2	1245	13	09YGH8

ALIGNMENTS

RESULT 1
ID 014953 PRELIMINARY; PRT; 884 AA.
AC 014953;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PROTEIN-TYROSINE KINASE.
GN BYK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE; 97318332.
RA KAJI Y., NINOMIYA D., KATO M., MIZUGUCHI M., SAJI M., KATSUMOTO T.,
RA OHNO K., TAKASHIMA S., ONODERA K.,
RT "A tyrosine kinase-like molecule is localized in the nuclear membrane
of neurons: hippocampal behavior under stress";
RL Biol. Cell 88:45-54(1996).
DR EMBL; D50479; BAA21781.1;
DR PRAM; PR00041; fn3; 2.
DR PRAM; PR00047; Ig; 2.
DR PRAM; PR00069; PKinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Tyrosine-protein kinase
SQ SEQUENCE 884 AA; 96179 MW; 624CDDA9 CRC32;

Query Match 51.3%; Score 2400; DB 4; Length 884;
Best local Similarity 95.9%; Pred. No. 7.9e-194;
Matches 466; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 382 SQDWDSTFVSVOQNSNPAMWVYVLTALVTAALALILRRRRETRFGQAF 441
DB 399 WSQPLVYSSSHDRAGQOGPHSRSTSVYVLTALVTAALALILRRRRETRFGQAF 458
QY 442 DSYMAGEPRVHPRARRSRNREPERIEATLDSLGISDELKEDVLIPEOQFTGRML 501
DB 459 DSYMAGEPRVHPRARRSRNREPERIEATLDSLGISDELKEDVLIPEOQFTGRML 518
QY 502 GKGEFSGVEAQLKQEDGFEVKAAYKMLKADIIASSDIEPFLREAAQMEPHPRVAKY 561
DB 519 GKGEFSGVEAQLKQEDGFEVKAAYKMLKADIIASSDIEPFLREAAQMEPHPRVAKY 578
QY 562 GYSLRRAGRLPIPVYVILPEKKGDLHAFLASRIGENPFNLPQTLIRFVYDIACGE 621
DB 579 GYSLRRAGRLPIPVYVILPEKKGDLHAFLASRIGENPFNLPQTLIRFVYDIACGE 638
QY 622 YLSRNFIRHDLAARNCMAEDMTVCVADFGLSRKTIYSDDIYRQGCASRLPVKMLAESL 681

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Db 639 YLSRRFIHDLAARNCHAEEDTTCVADGSLSKITSGDYTRQSGASKLPKWTALLES 698
Oy 682 ADNLTYVSDVMAFGVTMEIMTRGOTPYAGIENAEIYNLLIGNLAKOPPECEMEDVYL 741
Db 699 ADNLTYVSDVMAFGVTMEIMTRGOTPYAGIENAEIYNLLIGNLAKOPPECEMEDVYL 758
Oy 742 MIOCSADPKORPSFTCLMELENITLGSLSASODPLYINIERAEPTAGSLELPGR 801
Db 759 MIOCSADPKORPSFTCLMELENITLGSLSASODPLYINIERAEPTAGSLELPGR 818
Oy 802 DOPYSAGDGSAGMGAVGTPSDCRITLTPGGIAEPGQAEHPESPENLNTORLLLOOGL 861
Db 819 DOPYSAGDGSAGMGAVGTPSDCRITLTPGGIAEPGQAEHPESPENLNTORLLLOOGL 878
Oy 862 LPHSSC 867
Db 879 LPHSSC 884

TIT 2
/87
AC 012787 PRELIMINARY; PRT; 723 AA.
AC 012787;
DT 01-NOV-1996 (TRENBLREL 01, Created)
DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
DT 01-MAY-1999 (TRENBLREL 10, Last annotation update)
DE RECEPTOR TYROSINE KINASE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94151024.
RA DAI W., PAN H., HANDY H., GUPTA S.L., MURPHY M.J.;
RT "Molecular cloning of a novel receptor tyrosine kinase, tlf, highly
RT expressed in human ovary and testis."
RL Oncogene 9:975-979(1994).
DR EMBL; D02566; AAA17407.1; -.
DR PFM; PF00041; fn3; 2.
DR PFM; PF00069; PKinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
FT NON TER
FT SEQUENCE 723 AA; 78787 MW; B667D834 CRC32;

Query Match 50.0%; Score 2337.5; DB 4; Length 723;
est Local Similarity 92.98; Pred. No. 1.1e-188;
atches 461; Conservative 7; Mismatches 25; Indels 3; Gaps 3;

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Db 519 ADNLTYVSDVMAFGVTMEIMTRGOTPYAGIENAEIYNLLIGNLAKOPPECEMEDVYL 577
Oy 742 MIOCSADPKORPSFTCLMELENITLGSLSASODPLYINIERAEPTAGSLELPGR 801
Db 578 MIOCSADPKORPSFTCLMELENITLGSLSASODPLYINIERAEPTAGSLELPGR 637
Oy 802 DOPYSAGDGSAGMGAVGTPSDCRITLTPGGIAEPGQAEHPESPENLNTORLLLOOGL 861
Db 638 DOPYSAGDGSAGMGAVGTPSDCRITLTPGGIAEPGQAEHPESPENLNTORLLLOOGL 697
Oy 862 LPHSSC 877
Db 698 L-HYAVSPOERASGP 712

RESULT 3
ID 060752 PRELIMINARY; PRT; 876 AA.
AC 060752; 009080; 062482; P70285; 009070;
DT 01-NOV-1996 (TRENBLREL 01, Created)
DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
DT 01-MAY-1999 (TRENBLREL 10, Last annotation update)
DE TYROS3 PROTEIN TYROSINE KINASE 3
DE (PUTATIVE GROWTH FACTOR RECEPTOR TYROSINE KINASE ISOFORM B) (TYROS3)
GN TYROS3 OR ETK2/TYROS3
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE; 95240399
RA SCHULZ N., PAULHAC C., LEE L., ZHOU R.;
RT "Isolation and expression analysis of tyros3, a murine growth factor
RT receptor tyrosine kinase preferentially expressed in adult brain."
RL Mol. Brain Res. 28:273-280(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE; 94193774.
RA MARK M.R., SCADDEN D.T., WANG Z., GU Q., GODDARD A., GODOWSKI P.J.;
RT "tse, a novel receptor-type tyrosine kinase with homology to AxL/Ufo,
RT is expressed at high levels in the brain."
RL J. Biol. Chem. 269:10720-10728(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE; 94150990.
RA FUJIMOTO J., YAMAMOTO T.;
RT "Prl, a mouse gene encoding a novel receptor-type protein-tyrosine
RT kinase, is preferentially expressed in the brain."
RL Oncogene 9:693-698(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE; 97044738.
RA SASAKI M., ENAMI J.;
RT "Structure and expression of a murine homologue of sky receptor
RT tyrosine kinase gene."
RL J. Biochem. 120:264-270(1996).
RN [5]
RP SEQUENCE OF 1-88 FROM N.A.
RX STRAIN-129SV; TISSUE-LIVER;
RX MEDLINE; 95303487.
RA BRESCHER E.G., GIANNOLA D.M., EMERSON S.G.;
RT "Identification of alternative exons, including a novel exon, in the
RT tyrosine kinase receptor gene Etk2/tyros3 that explain differences in
RT 5' cDNA sequences."
RL Oncogene 10:2239-2242(1995).
RN [6]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C; TISSUE-BRAIN;

```


2X MEDLINE: 94150991.
 2A OHSASHI K., MIZUNO K., KUMA K., MIYATA T., NAKAMURA T.;
 2T Cloning of the cDNA for a novel receptor tyrosine kinase, Sky,
 2T predominantly expressed in brain.";
 2L Oncogene 9:699-705(1994).
 2N [1]

3N SEQUENCE FROM N.A.
 3C STRAIN-BALB/C;
 RA SASAKI M.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB000826; BAA19191.1;
 DR EMBL: AB000827; BAA19192.1;
 DR EMBL: U18343; AAB26943.1;
 DR EMBL: U23721; AAC52215.1;
 DR EMBL: U23718; AAC52215.1; JOINED.
 DR MGI: 104294; TYRO3.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00047; fn3; 2.
 DR PFAM: PF00069; PKinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 FT NON_TER 876 876
 SO SEQUENCE 876 AA; 96055 MW; 54D682DB CRC32;

Query Match 48.0%; Score 2246; DB 11; Length 876;
 Best Local Similarity 90.1%; Pred. No. 7,6e-181;
 Matches 438; Conservative 14; Mismatches 34; Indels 0; Gaps 0;

QY 382 FSDWMDSTFSVVOQNSNPANRANVPVVLGVLTALVTAAALILILRRKRETRFGQAF 441
 DB 391 WSGPLVSSHHDHAGRGPPHSRTSWPVVLGVLTALITAAALILILRRKRETRFGQAF 450
 QY 442 DSYMAGEPAVHFRARSRNRRPERIEATLDSIGSDLEKLEEDVLIPEQOFTLGRML 501
 DB 451 DSYMAGEPAVHFRARSRNRRPERIEATLDSIGSDLEKLEEDVLIPEQOFTLGRML 510
 QY 502 GGEFGSVREAOIKODGSEFVAVKMLKADIIASSDIEEFLREACKKEFDHPHYAKLY 561
 DB 511 GGEFGSVREAOIKODGSEFVAVKMLKADIIASSDIEEFLREACKKEFDHPHYAKLY 570
 QY 562 GVSLSRAGRLPIPVYIIPFKHGDHLAFLASRIGENFNLPLQTLIRFVWDIACGNE 621
 DB 571 GVSLSRAGRLPIPVYIIPFKHGDHLAFLASRIGENFNLPLQTLIRFVWDIACGNE 630
 QY 622 YSSSRFIRDLAARNCMAEDMTVCVADFGLSRKITYSGDYRQCASKLPYKWTALDSL 681
 DB 631 YSSSRFIRDLAARNCMAEDMTVCVADFGLSRKITYSGDYRQCASKLPYKWTALDSL 690
 QY 682 ADNLTYVSDVNAFVGTMEIMTRGOTPYAGIENAEIYNYLIGGNRLKOPPECKMEVYDL 741
 DB 691 ADNLTYVSDVNAFVGTMEIMTRGOTPYAGIENAEIYNYLIGGNRLKOPPECKMEVYDL 750
 QY 742 MYQCSADPKORPSTCLMELENILIGOLSVLASODPLYINIERAEPTAGSLELPER 801
 DB 751 MYQCSADPKORPSTCLMELENILIGOLSVLASODPLYINIERAEPTAGSLELPER 810
 QY 802 DOPYGAGDGSAGVAGTSPDCRYITLPGGL--AEOPQAHOEP--AEPQQAHOEP 861
 DB 811 ERSSSEADGDSGAVGAGIPDSRYIFSPGILSESPGOLEOPEPSPLENQRLILLQOGL 870
 QY 862 LPHSSC 867
 DB 871 LPHSSC 876

RESULT 4
 ID 062121 PRELIMINARY; PRT; 856 AA.
 AC 062121;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)

DE PROTEIN TYROSINE KINASE.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 94150990.
 RA FUJIMOTO J., YAMAMOTO T.;
 RT b'rt, a mouse gene encoding a novel receptor-type protein-tyrosine
 RT kinase, is preferentially expressed in the brain.";
 RL Oncogene 9:693-698(1994).
 DR EMBL: D17393; BAA04216.1;
 DR MGI: 104294; TYRO3.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00047; fn3; 2.
 DR PFAM: PF00069; PKinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 SO SEQUENCE 856 AA; 93930 MW; 2DEBFC84 CRC32;

Query Match 44.5%; Score 2080; DB 11; Length 856;
 Best Local Similarity 87.7%; Pred. No. 7,4e-167;
 Matches 408; Conservative 15; Mismatches 40; Indels 2; Gaps 1;

QY 382 FSDWMDSTFSVVOQNSNPANRANVPVVLGVLTALVTAAALILILRRKRETRFGQAF 441
 DB 390 WSGPLVSSHHDHAGRGPPHSRTSWPVVLGVLTALITAAALILILRRKRETRFGQAF 449
 QY 442 DSYMAGEPAVHFRARSRNRRPERIEATLDSIGSDLEKLEEDVLIPEQOFTLGRML 501
 DB 450 DSYMAGEPAVHFRARSRNRRPERIEATLDSIGSDLEKLEEDVLIPEQOFTLGRML 509
 QY 502 GGEFGSVREAOIKODGSEFVAVKMLKADIIASSDIEEFLREACKKEFDHPHYAKLY 561
 DB 510 GGEFGSVREAOIKODGSEFVAVKMLKADIIASSDIEEFLREACKKEFDHPHYAKLY 569
 QY 562 GVSLSRAGRLPIPVYIIPFKHGDHLAFLASRIGENFNLPLQTLIRFVWDIACGNE 621
 DB 570 GVSLSRAGRLPIPVYIIPFKHGDHLAFLASRIGENFNLPLQTLIRFVWDIACGNE 629
 QY 622 YSSSRFIRDLAARNCMAEDMTVCVADFGLSRKITYSGDYRQCASKLPYKWTALDSL 681
 DB 630 YSSSRFIRDLAARNCMAEDMTVCVADFGLSRKITYSGDYRQCASKLPYKWTALDSL 689
 QY 682 ADNLTYVSDVNAFVGTMEIMTRGOTPYAGIENAEIYNYLIGGNRLKOPPECKMEVYDL 741
 DB 690 ADNLTYVSDVNAFVGTMEIMTRGOTPYAGIENAEIYNYLIGGNRLKOPPECKMEVYDL 749
 QY 742 MYQCSADPKORPSTCLMELENILIGOLSVLASODPLYINIERAEPTAGSLELPER 801
 DB 750 MYQCSADPKORPSTCLMELENILIGOLSVLASODPLYINIERAEPTAGSLELPER 809
 QY 802 DOPYGAGDGSAGVAGTSPDCRYITLPGGL--AEOPQAHOEP--AEPQQAHOEP 844
 DB 810 ERSSSEADGDSGAVGAGIPDSRYIFSPGILSESPGOLEOPEPSPLENQRLILLQOGL 854

RESULT 5
 ID 055243 PRELIMINARY; PRT; 397 AA.
 AC 055243;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-JUN-1998 (Tremblrel. 06, Last annotation update)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
 GN GFR3.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 SO SEQUENCE FROM N.A.

RA WIDENFALK J., TOMAC A., LINDOVIST E., HOFER B., OLSON L.,
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA NAVEILHAN P., BAUDET C., MIKAELS O., SHEN L., WESTPHAL H.,
 RA ERNFORS P.,
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).
 DR EMBL: AF041842; AAC23558.1;
 DR EMBL: AF036163; AAC24468.1;
 SQ SEQUENCE 397 AA; 44302 MW; F77607CF CRC32;

Query Match 40.4%; Score 1888; DB 11; Length 397;
 Best Local Similarity 94.4%; Pred. No. 3.7e-151;

Matches 355; Conservative 5; Mismatches 10; Indels 6; Gaps 1;

QY 54 LEAGNSLATEENRFVNSTOARKKCEANPACAKAYOHLSGCTSSLSRPLPLESAMSADCL 113
 DB 25 LGAGNSLATEENRFVNSTOARKKCEANPACAKAYOHLSGCTSSLSRPLPLESAMSADCL 84
 DB 114 EAAEOLRNSSLIDCRCHRRKHOATCLDIYTVHPARSLGDELDVSPYEDVTYSKPMKM 173
 DB 85 EAAEOLRNSSLIDCRCHRRKHOATCLDIYTVHPARSLGDELDVSPYEDVTYSKPMKM 144
 QY 174 NLSKLNMLKPDSDCLKFAHMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOGRSFEKA 233
 DB 145 NLSKLNMLKPDSDCLKFAHMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOGRSFEKA 204
 QY 234 AESHAOGILLCCPCPEDAGCGERRNTIAPSCALPSTVPCNCLDRSFCRADPLCRSLMD 293
 DB 205 AESHAOGILLCCPCPEDAGCGERRNTIAPSCALPSTVPCNCLDRSFCRADPLCRSLMD 264
 QY 294 FQTHCHPMIILGTCATEOSRCIRAYLIGLTAMPNFIKVTVAALSCOTGSGNLODE 353
 DB 265 FQTHCHPMIILGTCATEOSRCIRAYLIGLTAMPNFIKVTVAALSCOTGSGNLODE 324
 QY 354 CEOLRSFSONPCLVEALAKKRFHOLFSDMDASTSVYQOONSMPAMRVVYIGV 413
 DB 325 CEOLRSFSONPCLVEALAKKRFHOLFSDMDASTSVYQOONSMPALR-----LDP 378
 QY 414 LTALVTAALALILR 429
 DB 379 RLPIISFILPILILQ 394
 RESULT 6
 ID 035325 PRELIMINARY; PRT: 397 AA.
 01-JAN-1998 (TREMblrel. 05, Created)
 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 01-AUG-1998 (TREMblrel. 07, Last annotation update)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
 GN GFR-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TRUPP M., RAYNSCHER C., IBANEZ C.F.,
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF020305; AAB70931.1;
 SQ SEQUENCE 397 AA; 44333 MW; F0C0C841 CRC32;

Query Match 40.4%; Score 1888; DB 11; Length 397;
 Best Local Similarity 94.4%; Pred. No. 3.7e-151;

Matches 355; Conservative 5; Mismatches 10; Indels 6; Gaps 1;

QY 54 LEAGNSLATEENRFVNSTOARKKCEANPACAKAYOHLSGCTSSLSRPLPLESAMSADCL 113
 DB 25 LGAGNSLATEENRFVNSTOARKKCEANPACAKAYOHLSGCTSSLSRPLPLESAMSADCL 84

QY 114 EAAEOLRNSSLIDCRCHRRKHOATCLDIYTVHPARSLGDELDVSPYEDVTYSKPMKM 173
 DB 85 EAAEOLRNSSLIDCRCHRRKHOATCLDIYTVHPARSLGDELDVSPYEDVTYSKPMKM 144
 QY 174 NLSKLNMLKPDSDCLKFAHMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOGRSFEKA 233
 DB 145 NLSKLNMLKPDSDCLKFAHMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOGRSFEKA 204
 QY 234 AESHAOGILLCCPCPEDAGCGERRNTIAPSCALPSTVPCNCLDRSFCRADPLCRSLMD 293
 DB 205 AESHAOGILLCCPCPEDAGCGERRNTIAPSCALPSTVPCNCLDRSFCRADPLCRSLMD 264
 QY 294 FQTHCHPMIILGTCATEOSRCIRAYLIGLTAMPNFIKVTVAALSCOTGSGNLODE 353
 DB 265 FQTHCHPMIILGTCATEOSRCIRAYLIGLTAMPNFIKVTVAALSCOTGSGNLODE 324
 QY 354 CEOLRSFSONPCLVEALAKKRFHOLFSDMDASTSVYQOONSMPAMRVVYIGV 413
 DB 325 CEOLRSFSONPCLVEALAKKRFHOLFSDMDASTSVYQOONSMPALR-----LDP 378
 QY 414 LTALVTAALALILR 429
 DB 379 RLPIISFILPILILQ 394
 RESULT 7
 ID 035118 PRELIMINARY; PRT: 397 AA.
 01-JAN-1998 (TREMblrel. 05, Created)
 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE GLIAL CELL LINE DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA 3
 GN GFR3 OR GFRALPHA-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL6; TISSUE-HEART;
 RX MEDLINE: 98205811.
 RA NAKANO S., ITO S., YANG L.-X., KIUCHI K.,
 RT "Molecular cloning and expression analysis of GFR alpha-3, a novel
 RT cDNA related to GDNF alpha and NTR alpha."
 RL Biochem. Biophys. Res. Commun. 244:849-853(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,
 RA POBESCU N.C., JOHNSON E.M. JR., MILBRANDT J.,
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).
 DR EMBL: AB008833; BAA23562.1;
 DR EMBL: AF051766; AAC24354.1;
 DR MDG: MGI:1201403; GFR3.
 SQ SEQUENCE 397 AA; 44307 MW; A80E0D24 CRC32;

Query Match 40.2%; Score 1880; DB 11; Length 397;
 Best Local Similarity 94.1%; Pred. No. 1.7e-150;

Matches 354; Conservative 5; Mismatches 11; Indels 6; Gaps 1;

QY 54 LEAGNSLATEENRFVNSTOARKKCEANPACAKAYOHLSGCTSSLSRPLPLESAMSADCL 113
 DB 25 LGAGNSLATEENRFVNSTOARKKCEANPACAKAYOHLSGCTSSLSRPLPLESAMSADCL 84
 QY 114 EAAEOLRNSSLIDCRCHRRKHOATCLDIYTVHPARSLGDELDVSPYEDVTYSKPMKM 173
 DB 85 EAAEOLRNSSLIDCRCHRRKHOATCLDIYTVHPARSLGDELDVSPYEDVTYSKPMKM 144
 QY 174 NLSKLNMLKPDSDCLKFAHMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOGRSFEKA 233
 DB 145 NLSKLNMLKPDSDCLKFAHMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOGRSFEKA 204

QY 224 AASHAGLLCCPCPEDAGCGERRRNTIAPSCALPSVTNCLDLSFCRADPLCRSLMD 293
 DB 205 AASHAGLLCCPCPEDAGCGERRRNTIAPSCALPSVTNCLDLSFCRADPLCRSLMD 264
 QY 294 FOTRHPMDILGTCTCTEBSRCLRAVLGLIGTAMTPEISKVTVAALSTCGSGNLDE 353
 DB 265 FOTRHPMDILGTCTCTEBSRCLRAVLGLIGTAMTPEISKVTVAALSTCGSGNLDE 324
 QY 354 CEOLERSFSONPCLEVEALIAAKRFRHOLFSDOMADSTSVQOONSAPKAWPVYLG 413
 DB 325 CEOLERSFSONPCLEVEALIAAKRFRHOLFSDOMADSTSVQOONSAPKAWPVYLG 378
 QY 414 LTAALTAALALILR 429
 DB 379 RLPLTSFSLPLILLQ 394
 RESULT 8
 1949
 Q98949 PRELIMINARY; PRT: 873 AA.
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE AXI-RELATED RECEPTOR TYROSINE KINASE.
 GN REK.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 97067156.
 RA BISCARDI J.S., DENNEZ F., BUEHLER G.F., CHESTNUT D.A., BARAGONA S.C.,
 O'BRYAN J.P., DER C.J., FRODOLIST J.J., FULTS D.W., MANESS P.F.,
 "Rek", a gene expressed in retina and brain, encodes a receptor
 tyrosine kinase of the AxI/Tyros family."
 RL J. Biol. Chem. 271.29049-29059 (1996).
 DR EMBL; U70045; AAC60041.1;
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00047; fn3; 2.
 DR PFAM; PF00069; PKinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 SQ SEQUENCE 873 AA; 96402 MW; 2918D550 CRC32;

Query Match 37.0%; Score 1728.5; DB 13; Length 873;
 Best Local Similarity 72.2%; Pred. No. 3.4e-137;
 Matches 346; Conservative 35; Mismatches 81; Indels 17; Gaps 4;

QY 386 MADSTFVVOO---QNSNPAMKAWPVYLGVTALVTAALALILRKRKKEFRGOAF 441
 DB 392 WSDFLLEADQVWGQOPPGTISWVVALGILVTAALALILRKRKKEFRGHAF 451
 QY 442 DSVMARGEPVHFAASFRERPERIEATLDSIGISDELKEXLEDVLIPOQOTLGRML 501
 DB 452 GSVVGRDPAVHRAASFRERPERIEATLDSIGISDELKEXLEDVLIPOQOTLGRML 511
 QY 502 GKKEFGSVRAQLKQEDGSFVKAVKMLKADIASDSIEELRENAKKEDEHPHAKV 561
 DB 512 GKKEFGSVRAQLKQEDGSFVKAVKMLKADIASDSIEELRENAKKEDEHPHAKV 571
 QY 562 GVSLSRAKRLPMPVILTFPMKGGDIAFLASRIGENPNPLQTLINPMVDIACME 621
 DB 572 GVSLSRAKRLPMPVILTFPMKGGDIAFLASRIGENPNPLQTLINPMVDIACME 631
 QY 622 YLSRNFHIDLAARNQMLAEDMTVCYADFGLSRKIRSGDYRGCASRLPYKWLAESE 681
 DB 632 YLSRNFHIDLAARNQMLAEDMTVCYADFGLSRKIRSGDYRGCASRLPYKWLAESE 691
 QY 682 ADNLVYQSVMAFGVYVMEIMTRGQTPYAGIENAEIYNTLIGNRKLKOPPECMEDVYL 741
 DB 692 ADNLVYQSVMAFGVYVMEIMTRGQTPYAGIENAEIYNTLIGNRKLKOPPECMEDVYL 751

QY 742 MYCKSADPKRPSFTCLRMELNIGLSTLSASODPLYNIRAE-----PTAGSL 796
 DB 752 MCRWHPKRLRPSFGVLRSLQLEMIRGMSTLSODPLYNICKDESSVDAVHTSF 811
 QY 797 ELPGDQYSGAGSGSGAVGTPSDCRITLTGGLAEDQGAHQHPESITNTQALL 855
 DB 812 GNTGDEETIAGA-----AAAITSDIRYIMSPCLGDDV-EGEHPGEGEGENKSL 862
 RESULT 9
 060609
 ID 060609 PRELIMINARY; PRT: 400 AA.
 AC 060609;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 DE GDNF FAMILY RECEPTOR ALPHA 3.
 GN GPR43.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BLOCH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,
 POPESCU N.C., JOHNSON E.M. JR., MIDBRANDT J.,
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0 (1998).
 DR EMBL; AF051767; AAC24355.1;
 SQ SEQUENCE 400 AA; 44538 MW; 6DFB5381 CRC32;

Query Match 33.5%; Score 1564; DB 4; Length 400;
 Best Local Similarity 75.8%; Pred. No. 8e-124;
 Matches 291; Conservative 27; Mismatches 56; Indels 10; Gaps 2;

QY 47 LPVLDQLLENGNSTATNREVNSTQARKKCEANPACKAAYOHGSCSTSLRPLLES 106
 DB 21 LPSPPLPLAGDPLPTESRLMNSCLARRKCOADPCSAVHHLDSCTSSISTPLPSEEP 80
 QY 107 AMSADCLAEAEQLNSSLIDCRCHRMKHQATLDIYTWHPARSLGDVLDVSPEDRY 166
 DB 81 SYPADCLAEAEQLNSSLIDCRCHRMKHQATLDIYTWHPARSLGDVLDVSPEDRY 140
 QY 167 TSXPKWKNLSKLNLRKPSDOLCFKFMALCTLHDKCDRLKRAYGEAGSGIRGCRHLCIAQ 226
 DB 141 TSXPKWKNLSKLNLRKPSDOLCFKFMALCTLHDKCDRLKRAYGEAGSGIRGCRHLCIAQ 200
 QY 227 RSFFERAAEHAAGLLCCPCPEDAGCGERRRNTIAPSCALPSVTNCLDLSFCRADPL 286
 DB 201 LTFEKKAEHFAAGLLCCPCPEDAGCGERRRNTIAPSCALPSVTNCLDLSFCRADPL 260
 QY 287 CSRRLMDFOHCHPMIDILGTCTEBSRCLRAVLGLIGTAMTPEISKVTVAALSTCGSG 346
 DB 261 CSRRLMDFOHCHPMIDILGTCTEBSRCLRAVLGLIGTAMTPEISKVTVAALSTCGSG 320
 QY 347 SGMLQDECEQLERSFSONPCLEVEALIAAKRFRHOLFSDOMADSTSVQOONSAPKAW 405
 DB 321 SGMLQDECEQLERSFSONPCLEVEALIAAKRFRHOLFSDOMADSTSVQOONSAPKAW 380
 QY 405 AMPVYVGLVLTATVTAALALIL 428
 DB 381 PWPVSLF-----SCTPLILL 396
 RESULT 10
 09Y166
 ID 09Y166 PRELIMINARY; PRT: 874 AA.
 AC 09Y166;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DEVELOPMENTAL RECEPTOR TYROSINE KINASE.
 GN DTK.

OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprininae; Rasbora; Danio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA WALSH J.A., JANSZ-PEREZ M., CROSIER K.E., EVANS C.W., CROSIER P.S.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF021344; AAD01694.1;
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 KW Receptor; Kinase.
 SO SEQUENCE 874 AA; 97599 MW; 17DC56DD CRC32;

Query Match 27.7%; Score 1297; DB 13; Length 874;
 Best Local Similarity 51.8%; Pred. No. 8.5e-101;
 Matches 287; Conservative 73; Mismatches 140; Indels 54; Gaps 13;

348 GNLDECEBOLERSF-----SONPCLVEAIAAK-----RFRHOLF----- 383
 329 GRQGEELRGLRLAYKLQWNGGSEODPLLFKEVVAHLGSGRFFNATFOVAAGTACGCGP 388
 QY 383 -SODMADSTFVYVQOONSPPANRAMPVYVLTALVTAALAILLRKRKRETCGOAF 441
 DB 389 WSPQVLYMVSMAOQTOR--GMMVGLLGLVATM-VGLLLIVLRNKGRTQFGSAF 445
 QY 442 DSVYARG-EPAYHFAARAFNRPERPERIATLDSIGISDELKEKEDVLIPIROQFLGSM 500
 DB 446 ---AAGGAVPYSTNARFNNQFPFLPESTLDSIGINDLAKDLVILFERLLTLGKM 502
 QY 501 LGGEGSVREAOIKOEDGSFVKAVAKMLKADIIASSDIEELREAAKKEEDHPHVAATL 560
 DB 503 LGGEGSVREAEFLKSENNSGQKVAVKLTQDINSSEDIQCKEAAVYKDPHHPVITOL 562
 QY 561 VGVLSRKAAGRLPIPMVILPFMKHGDHLAPILASRIGENPNPLQTLIRRVADIAGM 620
 DB 563 IGVSLHRAQORLPIPMVILPFMKHGDHLFTLMSRLGDEPTVSQQLIIFMLIARGM 622
 QY 621 EYLSRNFTHRDLAARNCLMADMTVCVADFGLSRKYSGDYRPGCASKLPVKMLAES 680
 DB 623 EYLSRNFTHRDLAARNCLMADMTVCVADFGLSRKYSGDYRPGCASKLPVKMLAES 682
 QY 681 LADNLYTQSDVWAGVYTMETITRQTPYAGIENAEIYNYLIGNRKLKQPECEDEYD 740
 DB 683 LADNLYTQSDVWAGVYTMETITRQTPYAGIENAEIYNYLIGNRKLKQPECEDEYD 742
 QY 741 LMYQCSADPKORSPFTCLMELENITIGQSLYLSASQDPLYNIR--AEETAG-GSIE 797
 DB 743 IMHSCSPYKCRPSFOHLIDOLELIMAKLNPAPYKEPLLNYNLEEDGEGQANSSTRSSE 802
 QY 798 LGRDQPYSGAG-----DQSGMAGVGTSPDCRYILTP--GGLAEPQCAEHQ 843
 DB 803 EPSWGVPMQCAIEDEDEKMLWVSSGAL-AIGG---DRIYITGVSVAIDESHSEHG 858
 QY 844 PPSPLNTEQORLLLL 857
 DB 859 LSEDIREEEDVIT 872

RESULT 11
 012866 PRELIMINARY; PRT; 999 AA.

AC 012866
 DT 01-NOV-1996 (TRENDArel. 01, Created)
 DT 01-NOV-1996 (TRENDArel. 01, Last sequence update)
 DT 01-AUG-1999 (TRENDArel. 11, Last annotation update)
 DE CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR (C-MER).
 GN C-MER.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Euteleostei; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD LEUKOCYTES;
 RX MEDLINE; 94368701.
 RA GRAHAM D.K., DAWSON T.L., MULLANEY D.L., SNOODGRASS H.R., EARP H.S.;
 RT "Cloning and mRNA expression analysis of a novel human protooncogene,
 RT Cell Growth Differ. 5:647-657(1994).
 RL [2]
 RN ERRATUM.

RA GRAHAM D.K., DAWSON T.L., MULLANEY D.L., SNOODGRASS H.R., EARP H.S.;
 RL Cell Growth Differ. 5:1022-1022(1994).
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC THE EXTRACELLULAR DOMAINS CONTAINS 2 IG-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

DR EMBL: U08023; AAB60430.1;
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PFM: PF00041; In3; 2.
 DR PFM: PF00041; In3; 2.
 DR PFM: PF00069; pkinase; 1.

KM Proto-oncogene; Transmembrane; Repeat; Immunoglobulin domain; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 999
 FT DOMAIN 19 501
 FT DOMAIN 90 182
 FT DOMAIN 198 266
 FT DOMAIN 283 372
 FT DOMAIN 376 480
 FT TRANSMEM 502 518
 FT DOMAIN 519 999
 SO SEQUENCE 999 AA; 110390 MW; 20274ED6 CRC32.

Query Match 24.7%; Score 1155.5; DB 4; Length 999;
 Best Local Similarity 38.8%; Pred. No. 8.9e-89;
 Matches 294; Conservative 115; Mismatches 207; Indels 141; Gaps 27;

233 AAESH-----AAGILL-----CQPPEDAGCGERRRTIPSCALPVS-----TP--N 273
 DB 261 SCEANDKGLVSGQVQINAIKPSPEVSI-----KSTHSLITISVWPFEDGSPFRN 316
 QY 274 C-LDIRSCADPLCRSLMDFOCHCPMDLIGTCATQOSCLRAY-----LGLIG-TA 325
 DB 317 CSIQVK---EADPLNGSVMIFFTSALP---HLQIQQLALNYSIGVSCMEIGISA 369
 QY 326 MTP-----NFISVNTVAL-----SCTCRGS 347
 DB 370 VSPWILASTTEGAPSVAPLNTVFLNESSDNDVIRWMPKPTKODGELVGRISHVQSA 429
 QY 348 GNLDECEBOLERSFQ-----NPLVEAIAAKMRHRLFS-----QDMAD-S 389
 DB 430 GISELLEEVQONSRRARISVQVHNACTVRIAAVTRGVGPFSDPVKIFIPAGWVDA 489
 QY 390 TFSVYVQOONSPPANRAMPVYVLTG-----VLTALVTAALAILLRKRKRETCGOAF--- 442
 DB 490 PPSYPAPGNADP-----VLIIFGCGFILLGLIYLSLA---IRKQVEKRFNAPTEE 541
 QY 442 DSVYARGEPAYHFAARAFNRPERPERIATLDSIGISDELKEKEDVLIPIROQFLGSM 501
 DB 542 DS-----ELVNYTAKSFCR---RAIETLHSGVGESELOKNEDEVDIDRNLLITKIL 593
 QY 502 KGEGSVREAOIKOEDGSFVKAVAKMLKADIIASSDIEELREAAKKEEDHPHVAATL 561
 DB 594 GEGFEGSVMEGNLKQEDGTSIKAVAKMLKADINSRHEIEELSLAACKQDSHNVIRLL 653
 QY 562 GVSLSRAKGRPLPIPMVILPFMKHGDHLAPILASRIGENPNPLQTLIRRVADIAGM 621
 DB 654 GVCIEKSSQG-IPRPVILPFMKHGDHLFTLMSRLGDEPTVSQQLIIFMLIARGM 712
 QY 622 YLSRNFTHRDLAARNCLMADMTVCVADFGLSRKYSGDYRPGCASKLPVKMLAESL 681
 DB 713 YLSRNFTHRDLAARNCLMADMTVCVADFGLSRKYSGDYRPGCASKLPVKMLAESL 772

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QY 682 ADLVLYVSOVAFVGTMTMEINTRGCPYVAGIEAYNTLIGNRLLKOPPEMEDVDYL 741
DB 773 ADVAVYSKSDVAFVGTMTMEINTRGMTPIYGVONHEMTDYLLHGHRLKOPEDCDLDEYET 832
QY 742 MYOCSADPRKPRSFCTCLARELENITIGOLSVLSASODPLYN--TERAEPTAGSGL-E 797
DB 833 MYSCMTDPLDRFTFSVLRQLQELLESPLDVANQADVITYVNOULESSGGLAQPTLAF 892
QY 798 LGRDQPYGAGDGSQMGAVG-----GTPDCRYITLPGG----LAOPGOAHOH 844
DB 893 LQNLNIDPDSIIASCTPRRAISVYTAEVHDSKPEHGRITLNGSGEEMEDLTSAPSAVTA 952
QY 845 ESPLNETORLL-----LLOGLPHSSCADASIKMD 876
DB 953 KNSVLPGERLVNRGVSWSHSKMLPLGSSLDPELTFAD 989

RESULT 12
062194 PRELIMINARY; PRT; 511 AA.
062194:
DR 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DI 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE RECEPTOR PROTEIN-TYROSINE KINASE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN-CD-1; TISSUE-TESTIS;
RA DOWDS C.A., BURKS D.J., SALING P.M.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; L1625; AAA85355.1;
DR PIRAM; PF00069; pkinase; 1.
KW Tyrosine-protein kinase.
FT NON TER
SQ SEQUENCE 511 AA; 57410 MW; 401B1C3A CRC32;

Query Match 24.5%; Score 1146; DB 11; Length 511.
Best Local Similarity 50.2%; Pred. No.2,1e-88;
Matches 246; Conservative 77; Mismatches 121; Indels 46; Gaps 13.

QY 409 VVLG-----VLTALVTAALALILLRKRRTRFQGA--DSYARGPAYHFRARSF 460
DB 28 ILGCFGCGFILGLILCVSLA--LRRAVETKFGGAFSEDSQL-----VNYRAKKKF 79
461 NNERERIEATIDSGIDELKEKEDVLIPIQOFTLKMGLKGEGSVREKQLOEDGS 520
DB 80 CR--RALELTQSGVSEELONKEDVYIDNLLVLTGLVLEGEFGSVMEGNLKOEDGT 136
QY 521 FVKVAVKMLKADIIASDDEEFLRPAACKPEEDHPVAVLVAVSLRSRAKGLPIPMYL 580
DB 137 SQKVAVKMKLDNFSQRETEEFSLSLACKKDNHNRNVTLLGVCTELSSQG-IPKPMYL 195
QY 581 PPKAKGDIAFLTASRIGENFPNLPQTLIRFVVDIACGMEXLSRNFTHRDIAARNCL 640
DB 196 PFMKRGDHLTEFLYRLMTGPRYIHLQTLKFMADIAQGMEXLSRNFTHRDIAARNCL 255
QY 641 AEDMNVCAVDELRSKRITSGDYVYRGGCASKLPVKTLALESADNLITYOSDVMAFGVTM 700
DB 256 RDDMNVCAVDELRSKRITSGDYVYRGGCASKLPVKTLALESADNLITYOSDVMAFGVTM 315
QY 701 EIMRTGQTPYAGIEAETLYNYLIGNRLLKOPPECKEDVDYLKYOCMSADPRKPSFTCLR 760
DB 316 EITRTGKMTPIYGVONHEMTDYLLHGHRLKOPEDCDLDEYDITSCMSADPLDRPTFSVLR 375
QY 761 MELENITIGOLSVLSASODPLYNIRAE--EPTAGGSLELPGRD--OPIYGAGDGSQMG 815
DB 376 LQLEKTLSESLPDADOKESIIYINTQLTLESCEGIANGP-SLTGLDNINIDPDSIIASCTPGA 434
QY 816 AVGGPSPSC-----HYILLPGGLADPGQAEHQPSPLNEITRLLILQOGLLPHSSC 867

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Db      435 AVSVTAETHENNRREERYTLNCGN--EEMEDVSSPPFAAYTPE-----KQGVLEETD- 486
OY      868 ADASLKMAPD 877
Db      486 ---SPKMASP 492

RESULT 13
060805 PRELIMINARY; PRT; 994 AA.
ID 060805;
AC 060805;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-NOV-1996 (TREMBLrel. 08, last annotation update)
DR C-MER PROTOONCOGENE, PRECURSOR (C-MER TYROSINE KINASE RECEPTOR).
GN MER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
   Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE OF 1-315 FROM N.A.
RC STRAIN-B6; TISSUE-SPLEEN;
RX MEDLINE; 95303502.
RA GRAHAM D.K., BOWMAN G.W., DAWSON T.L., STANFORD W.L., EARP H.S.,
RA SNODGRASS H.R.;
RL "Cloning and developmental expression analysis of the murine c-met
   tyrosine kinase."
RL Oncogene 10:2349-2359(1995).
RN [2]
RS SEQUENCE FROM N.A.
RA STRAIN-B6; TISSUE-SPLEEN;
RA SNODGRASS H.R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DL EMBL; UZ1501; AAA80222.1; .
DR DR MGD; MGI:96965; MER.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00047; lgf; 2.
DR PFAM; PF00069; ptinase; 1.
KW signal.
FT SIGNAL.
FT CHAIN 1 20 POTENTIAL.
FT FT 21 994 C-MER TYROSINE KINASE RECEPTOR.
SO SEQUENCE 994 AA; 110156 MW; 3CD2F429D CRC32;

Query Match 24.3%; Score 1137; DB 11; Length 994;
Best Local Similarity 53.2%; Pred. No. 3.2e-87;
Matches 236; Conservative 71; Mismatches 103; Indels 34; Gaps 10;

OY 409 VILG-----VTALVTAAALAILLRKRKRKEFGCAF---DSVARGGPAYHFAARSF 460
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 499 IILGCFCCFILIGLICISLA---LRRVOETKFSGAISEEDSOL----VNYTRAKSF 550
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 461 NREREERIEATLDISGISDELDEKLEDVLIPROPTFLRMKGEGFSVREALKOEDEGS 520
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 551 CR---RAIELTQLSGVSEELKONKLEDEVIVDRNLTVLGKYLGESEGFSGMEGNLKQDEGT 607
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 521 FVKYAVVKMLKADIIASSIIEFFLRPAACMKEPDHVAKYGLYSLSRAKGRPLTPAYIL 580
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 608 SQKAAYVMKMDNSQSRIEEFLSEAAKCMKFNHPNVIRLLGVCIETLESQG-IKPPAVIL 666
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 581 PFMRHGDIHAFLIASRIENPFNPLOTLIFPMVDIAGMETSRRNFTHIDLARNOML 640
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 667 PFMYGDLHTLLSLRMTGPXYITLQTLTFMADIAGMEYLSKNFLHRDLARNCML 726
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 641 AEDKTCVADFGLSKRTIYSGDYRQGCASKLPVKWLALESADNLYTYQSDYMAFGVTMM 700
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 727 RDMWTVCADDFGLSKRTIYSGDYRQGRIRAKMPVKWIAIESLADRYITSKDPVAFGTMM 786
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 701 ELIMRGOPPYVGINSNAETYNLLIGGNRLKOPPECMEDVYDLMQCRMSADPKQRSFTCLR 760
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
OY 787 ELTRGMATPIPGVONHEMYDILLGHGRKOFECDCLEDELYDINTSCWSADPLDRPTFSYLR 846
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

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QY 761 MELENIIGOLSVLSASODPLYINIERAE---EPTAGSLPEGRD---QPSGAGDSGSG 815
DB 847 LQLEKLESIPDADKESITIIYNQLESCEGLANGP-SLTGDMNDIPSIISCTPGA 905
QY 816 AVGTGSDC-----RYLTTPG 831
DB 906 AVSVTAVEHNNLRERYILNG 929

RESULT 14

QY 090777 PRELIMINARY; PRT; 974 AA.
AC 090777;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
DE C-EYK PROTO-ONCOGENE PROTEIN PRECURSOR.
GN C-EYK.
OS Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 94124527.
RA JIA R., HANAFUSA H.;
RT "The proto-oncogene of v-eyk (v-tyk) is a novel receptor-type protein
tyrosine kinase with extracellular Ig/GN-III domains."
RL J. Biol. Chem. 269:1839-1844(1994).
DR EMBL; L21719; AAC38010.1;
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00047; fn3; 2.
DR PFAM; PF00069; pkinase; 1.
KM Signal.
FT SIGNAL. 1 23 POTENTIAL.
FT CHAIN 24 974 C-EYK PROTO-ONCOGENE PROTEIN.
SQ SEQUENCE 974 AA; 106165 MW; E26ED23 CRC32;

Query Match 23.6%; Score 1102.5; DB 13; Length 974;
Best Local Similarity 48.2%; Pred. No. 2.5e-84;
Matches 235; Conservative 75; Mismatches 141; Indels 37; Gaps 9;

QY 409 VVLTALVTAAAL---ILRRKRTFRGOAF---DSVAREPVAHRAARSEFR 462
DB 494 VALGFCGV-ANGILCSVIOKCMETKGNASRND---ELVYNTAKSYCR 547
463 ERPERLEATLDSIGDELKEDVLIPEOFTLGRMLKGEFGSVREAOIKOEDGSFV 522
548 ---RAVELTIGSVSELQKLOVDVDRNALSLGKVLGESEFGVMGRSLQSEGTQ 604
QY 523 KVAVKRLKADITASSIEEFLREDAKMEFDPHVAKLVSLSRANGRLPIPVILPF 582
DB 605 KVAVKRLKADITASSIEEFLREDAKMEFDPHVAKLVSLSRANGRLPIPVILPF 582
583 MKHGDLAFLASRGENFNPLOTILRFMDIAGMEYSSRNFIHDLAARCMAL 642
DB 664 MKYGDHSLSLSRLEMAFQVPLQMLTFMDVILGMEYSSROFLHDLAARCMAL 723
QY 643 DMTVCVADGSLSRKITYSGDYRQGCASKLPRVLALESIALDNLTYVQSDVAFVTAMEI 702
DB 724 DMTVCVADGSLSRKITYSGDYRQGCASKLPRVLALESIALDNLTYVQSDVAFVTAMEI 702
QY 703 MKRGOTPAGINAETIYNLIGNRLKOPPECEMEVDYDLMQCVADKORPSFTCLME 762
DB 784 MKRGOTPAGINAETIYNLIGNRLKOPPECEMEVDYDLMQCVADKORPSFTCLME 762
784 MKRGOTPAGINAETIYNLIGNRLKOPPECEMEVDYDLMQCVADKORPSFTCLME 762
QY 763 LENIGOLSVLSASODPLYINIERAE-----PTAGSLPEGRDPIYSGA 808
DB 844 LQLEKLESIPDADKESITIIYNQLESCEGLANGP-SLTGDMNDIPSIISCTPGA 905
QY 809 GDGSGMAGVGTPSDCRITLPGGLAEPGAERHOPESPLNETQRLILLOGLPHSSCA 868

DB 903 HKRALVAVDHIDGGRVYL-----ESGSEPTEDAYVPLPHEGSAMTEASTLPVGS 956
QY 869 DASLKVAD 876
DB 957 AAOPLCAD 964

RESULT 15

QY 015516 PRELIMINARY; PRT; 600 AA.
AC 015516;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1998 (TRENBLREL. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
DE TYROSINE KINASE.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE; 95327955.
RA BURKS D.J., CARBALLADA R., MOORE H.D., SALING P.M.;
RT "Interaction of a tyrosine kinase from human sperm with the zona
pellucida at fertilization."
RL Science 269:83-86(1995).
DR EMBL; L08961; AAC41766.1;
DR PFAM; PF00069; pkinase; 1.
KM Transmembrane.
SQ SEQUENCE 600 AA; 67874 MW; 54C9ACB0 CRC32;

Query Match 17.3%; Score 811; DB 4; Length 600;
Best Local Similarity 41.6%; Pred. No. 4.8e-60;
Matches 215; Conservative 73; Mismatches 125; Indels 104; Gaps 25;

QY 333 KYNTVALSC-----TCRG-SGNLQDCEOLERSFSON--PCLVEATAKRRFR- 380
DB 96 KINTLHIPCGRGPQNPNTCRDLKCNVSD---YORAMPGNVTC-----TRRL 144
QY 380 -QLF-SQOMASTFEVQOQNSNPRKRVVVLGVLTALYTAALAILLKRKRETF 437
DB 145 CPLENSGM-----ORRSCAHMLMLMI-ILGLVLYSLA---TRKRVQETKF 190
QY 438 GOAF---DSVAREPVAHRAARSEFRPERLEATLDSIGDELKEDVLIPEOQ 494
DB 191 GNAFTEDS-----ELVYNTAKSYCR---RAIELT-HSLGVSEELONKLEVDVDRNL 241
QY 435 FTGLMLKGEFGSVREAOIKOEDGSFVK--VAVKMLRADIIASDIEFLREDAKMEF 552
DB 242 LILGKILDEGEKGVYEGILMNIPEGEVKIPVAKTKLIDTMAN---KEILDEASVMKG 298
QY 553 DHPVAKIYVGLSLSRKAGRLPIPVILPEKRGDLAFLASRGENFNPLOTILRF 612
DB 299 GNPVAKIYVGLSLSRKAGRLPIPVILPEKRGDLAFLASRGENFNPLOTILRF 612
QY 613 MYDIAGMEYSSRNFIHDLAARCMALDEPTCVADFGSLRITYSGDYRQGCASKL 672
DB 354 MYDIAGMEYSSRNFIHDLAARCMALDEPTCVADFGSLRITYSGDYRQGCASKL 672
QY 673 VKTALLESIALDNLTYVQSDVAFVTAMEINT--RGOTPAGINAETIYNLIGNRLK 730
DB 414 VKTALLESIALDNLTYVQSDVAFVTAMEINT--RGOTPAGINAETIYNLIGNRLK 730
QY 731 PP---ECME-----DYIDL-----MYQMSAD---PK 751
DB 473 PRTAMNCTEIRILKLPITIGSRTRMPTITFSMTATRSPTAMNCKKCTLAGEBIPK 532
QY 752 ORPSFTCLMELENIIGOLSVLSASODPLYINIERAE 788
DB 533 TGPTFSVLRQLKLESIPDADKESITIIYNQLESCEGLANGP-SLTGDMNDIPSIISCTPGA 905

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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:20:29 ; Search time 33.26 Seconds

(without alignments)
679.590 Million cell updates/sec

Title: US-09-272-835-17

Sequence: 1 MVRPLNRPPLPPVYLMILL.....PWPSLFSCTLPILLLSLM 369

Scoring table: BLOSUM62

Searched: 199794 seqs, 61255205 residues

Database:

SPTREMBL_11.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1993.5	98.6	400	4 060609	060609 homo sapien
2	1458	72.1	397	11 035118	035118 mus musculu
3	1455	72.0	397	11 055243	055243 mus musculu
4	1453	71.9	397	11 035225	035225 mus musculu
5	514	25.4	464	11 035977	035977 rattus norv
6	509	25.2	464	4 015316	015316 homo sapien
7	509	25.2	464	4 015328	015328 homo sapien
8	488	24.1	460	4 015507	015507 homo sapien
9	487	24.0	463	11 035252	035252 mus musculu
10	485.5	24.0	465	4 043912	043912 homo sapien
11	485.5	24.0	468	11 035246	035246 mus musculu
12	485	24.0	463	11 035748	035748 rattus norv
13	470	23.2	431	13 093512	093512 gallus gall
14	410	20.3	358	11 092243	092243 mus musculu
15	410	20.3	330	11 092242	092242 mus musculu
16	147.5	7.3	2704	5 097458	097458 drosophila
17	141	7.0	2653	5 025253	025253 lucilia cup
18	131	6.5	2195	5 020462	020462 caenorhabd
19	123	6.1	2026	4 000468	000468 homo sapien
20	122.5	6.1	1964	11 035442	035442 mus musculu
21	121	6.0	3857	11 088840	088840 mus musculu
22	118.5	5.9	1989	4 099940	099940 homo sapien
23	118.5	5.9	2003	4 000306	000306 homo sapien
24	118.5	5.9	955	4 099466	099466 homo sapien
25	114.5	5.7	850	4 095804	095804 homo sapien
26	113.5	5.6	1034	11 035888	035888 rattus norv
27	111.5	5.5	1095	11 060784	060784 mus musculu
28	111	5.5	2019	11 064706	064706 mus musculu
29	110.5	5.5	5376	11 088799	088799 mus musculu

30	109	5.4	1661	5 077244	077244 chlorohydra
31	109	5.4	1203	11 006008	006008 mus musculu
32	109	5.4	4545	11 061291	061291 mus musculu
33	109	5.4	2470	11 035516	035516 mus musculu
34	108.5	5.4	2150	5 044131	044131 caenorhabd
35	107.5	5.3	1254	13 097402	097402 brachydanio
36	107	5.3	1792	13 057484	057484 gallus gall
37	106	5.2	838	5 018482	018482 opiliatasp
38	105.5	5.2	473	5 025464	025464 mytilus gal
39	105	5.2	448	4 075965	075965 homo sapien
40	104.5	5.2	3507	5 023587	023587 caenorhabd
41	104	5.1	1722	5 019350	019350 caenorhabd
42	103.5	5.1	2352	5 061240	061240 halocynthia
43	103.5	5.1	1296	5 022452	022452 caenorhabd
44	103.5	5.1	2531	5 016004	016004 lytechinus
45	103	5.1	1704	5 094446	094446 chironomus

ALIGNMENTS

RESULT 1
ID 060609 PRELIMINARY; PRT; 400 AA.
AC 060609;
DT 01-AUG-1998 (TRENBERG, 07, Created)
DT 01-AUG-1998 (TRENBERG, 07, Last sequence update)
DT 01-AUG-1998 (TRENBERG, 07, Last annotation update)
DE GDNF FAMILY RECEPTOR ALPHA 3.
GN GFR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,
RA POBESCU N.C., JOHNSON E.M. JR., MILBRANDT J.,
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).
DR EMBL: AF051767; AAC2435.1;
SQ SEQUENCE 400 AA; 44538 MW; 6DFB5381 CRC32;

Query Match 98.6%; Score 1993.5; DB 4; Length 400;
Best Local Similarity 92.0%; Pred. No. 9.3e-195;
Matches 368; Conservative 1; Mismatches 0; Indels 31; Gaps 1;

QY 1 MVRPLNRPPLPPVYLMILLPPSPPLAAGDPLTESRLMNSCLARRKQADPTCSAA 60
Db 1 MVRPLNRPPLPPVYLMILLPPSPPLAAGDPLTESRLMNSCLARRKQADPTCSAA 60
QY 61 YHNDSTSSISTPBPSEPSVPADCLAAQOLRNSLSIGCMCHRRKKNQVACLDITWTY 120
Db 61 YHNDSTSSISTPBPSEPSVPADCLAAQOLRNSLSIGCMCHRRKKNQVACLDITWTY 120
QY 121 HRAKSL-----DSOLCKFAMLTINDKCRRLK 149
Db 121 HRAKSL-----DSOLCKFAMLTINDKCRRLK 149
QY 150 AYEGACGPHCQHRVCLKOLLTFEERKAEPHAGLLCPCAPDRGCGERRRTIPNCA 209
Db 150 AYEGACGPHCQHRVCLKOLLTFEERKAEPHAGLLCPCAPDRGCGERRRTIPNCA 209
QY 181 AYEGACGPHCQHRVCLKOLLTFEERKAEPHAGLLCPCAPDRGCGERRRTIPNCA 240
Db 181 AYEGACGPHCQHRVCLKOLLTFEERKAEPHAGLLCPCAPDRGCGERRRTIPNCA 240
QY 210 LPPVAPNCLRLRCLFSDPLCRRLVDFQTHCHPMIDILGTCATGSRCLRAYIGLTGM 269
Db 210 LPPVAPNCLRLRCLFSDPLCRRLVDFQTHCHPMIDILGTCATGSRCLRAYIGLTGM 269
QY 241 LPPVAPNCLRLRCLFSDPLCRRLVDFQTHCHPMIDILGTCATGSRCLRAYIGLTGM 300
Db 241 LPPVAPNCLRLRCLFSDPLCRRLVDFQTHCHPMIDILGTCATGSRCLRAYIGLTGM 300
QY 270 TPVFSVNTSVALLSCGSGNLOEGCEMLBEGFSHNCPFAIAKKRFSOLFSDQM 329
Db 270 TPVFSVNTSVALLSCGSGNLOEGCEMLBEGFSHNCPFAIAKKRFSOLFSDQM 329
QY 301 TPVFSVNTSVALLSCGSGNLOEGCEMLBEGFSHNCPFAIAKKRFSOLFSDQM 360
Db 301 TPVFSVNTSVALLSCGSGNLOEGCEMLBEGFSHNCPFAIAKKRFSOLFSDQM 360
QY 330 PPHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLM 369
Db 330 PPHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLM 369
QY 361 PPHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLM 400
Db 361 PPHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLM 400

DE 01-JUN-1998 (TEMBLrel. 06, last annotation update)
DR GLIAL CELL LINE-DERIVED NEUROPHILIC FACTOR RECEPTOR ALPHA-3
GN GFAP3.
OS Mus musculus (Mouse).
OC Eutherozoa; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA WIDENALK J., TOMAC A., LINDOYIST E., HOFER B., OLSON L.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA NAVEILHAN P., BAUDET C., MIKAELS O., SHEN L., WESTPHAL H.,
RA ERNFORS P.;
RA Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).
DR EMBL: AF041842; AAC23558.1; -
DR EMBL: AF036163; AAC24468.1; -
SO SEQUENCE 397 AA; 44302 MW; F77607CF CRC32;

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0Y 5 LNRPRLPEVYVLMLELLLPSPPLPLAGDPLETSKLNNSCLQARKKCOADPTCSAAAYVHHT 64
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
Db 3 LSPERRP - LMTLLLVLSLMTPLGAGNSLMTENRFVNSQARKKKEANPACKAAYQH 61
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
0Y 65 DSCSSSLSTPLPEEESVADCLLEAAQOLRNSSLGLGCHCRMRKNQVACLDIYTVHRRAR 12
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
Db 62 GSCSSSLSRPLPEESAMADCLLEAAQOLRNSSLIDLCRHRMRKNQATCLDIYTVHRRAR 12
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :

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RESULT	4		
ID	035325		
AC	035325	PRELIMINARY:	PRT: 397 AA.
DT	01-JAN-1998	(TREMBLrel. 05, Created)	
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)	
DT	01-AUG-1998	(TREMBLrel. 07, Last annotation update)	
DE	G1AL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.		
GN	GFRA-3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	GROUP M. RAYNOSCHER C., IBANEZ C.F.;		
RL	Submitted (AUG-1997) to the EMBL/GenBank/DBD databases.		
QD	EMBL: AF020305; AAB:0931.1;		
SD	SEQUENCE 397 AA: 44333 MW: F0C0C841 CRC32;		

Query Match 71.9% ; Score 1453; DB 11; Length 397;
Best Local Similarity 69.9%; Pred. No. 7.6e-140;
Matches 274; Conservative 29; Mismatches 57; Indels 32; Gaps

OY 9 PLPPVLMILLPLPSPFLPAAGDPLETESRLKMSCLQARRKOADPTCSAAVHHDSCT 68
| | : | | | | : | | : | | : | | : | | : | | : | | : | |
DB 7 PRFP-LIMILLVLSTWLPFGAGNSLATERNFVNSTQAARKCEANAPCAAYOHGSGCT 65
OY 69 SSISTPLPSEBPVPADCLEAQQLRNSSLIGCGCHRRMKNOVAICLDIYTVARASL-- 127
| | : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 66 SSSIRPLPLESAMSADCLAEAQLRNSSLIDRCCHRMRKHQATCDLIYTWHPARSLD 125.
OY 127 -----DSDLCIFAMICTANDXCRIKKAYGCACGG 157
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 126 YELDVSYEDTYSKPKMNLISKLNMLKPSSDICLFAMICTLHDCDLRKAYGCACGG 185
OY 158 PHCRHYVCINQLITFEKEAPEAPHOGGLLPCCAPNRGCCERRRNTAPNCALPPAAPNC 217
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 186 IROCRHLCLNQLSRFEEKAPEAHQGILLCPCPEDAGCCERRRNIAASCALPSVTYPC 245
OY 218 LEHRLLCSDPLCRSLVDFTQHCPMDLIGTCATQSRLRAYLGILGTAMPNFVSNY 277
| | : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 246 LDRSFECRADPLRSRLMDFTQHCPMDLIGTCATQSRLRAYLGILGTAMPNFVSNY 305
OY 278 NTSVALSCTRGGNGNOEEMLEGFSHNHCLETIAAKRMFRHSOLFESODPHPFAYM 337
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 306 NTIVALSCTRGGNGNOEEMLEGFSHNHCLETIAAKRMFRHSOLFESODPHPFAYM 365
OY 338 AHONENPAVRPOPWPVPSLEFCPLPLLISLWM 369
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 366 QQONSNPALRLQPRLPILSRSLIPLLILOTM 397

RESULT 5
O35977 PRELIMINARY; PRT: 464 AA.

ID O35977 AC O35977:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JUN-1998 (TREMBLrel. 05, last sequence update)
DT 01-AUG-1999 (TREMBLrel. 11, last annotation update)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA (GDNF RECEPTOR-BETA).
GN GDNER-BETA OR RET12.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Rattus.
[1]
SEQUENCE FROM N.A.
RP TROPP M., RAYNOSCHER C., IBANEZ C.F.;
RN Submitted (Jul-1997) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RP TISSUE-BRAIN/KIDNEY;
RC TISSUE-BRAIN/KIDNEY;
RX MEDLINE: 97322356.
RA SANTOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C., WALUS J., ROBINSON S., JAWORSKI G., WEI H., TIARD R., WHITY A., PEPIŃSKY R.B., CATÉ R.L.;
RA "Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins."
RT Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
RN [1]

[3]
SEQUENCE OF 1-444 FROM N.A.
RP TISSUE=BRAIN/KIDNEY;
RA SANTOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C., WALUS J., ROBINSON S., JAWORSKI G., WEI H., TIARD R., WHITY A., PEPIŃSKY R.B., CATÉ R.L.;
RN Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE OF 1-444 FROM N.A.
RP TISSUE=HIPOCAMPLUS;
RA SUVALATO P., VARTIOVABARA K., LINDAHL M., MOSHTAKOV M., ARNE U., HOVENI-KITTUEN N., AIRAKSINEN M.S., PALOTIE A., SAARMA M., "Cloning, mRNA distribution and chromosomal localization of the gene

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RT      for glial cell line-derived receptor beta, a homolog to
RT      GDNF-alpha."
RL      Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF005226; AAB62247.1;
DR      EMBL; U97143; AAC53301.1;
KW      EMBL; AF003825; AAD09310.1;
SQ      RECEPTOR
SQ      SEQUENCE 464 AA; 51668 MW; B1A2BD11 CRC32;

Query Match
Best Local Similarity 25.4%; Score 514; DB 11; Length 464;
Matches 114; Conservative 38; Mismatches 113; Indels 58; Gaps 8

OY 44 CQARRKCOADPTCSAAVYHLDSCTS--SISTPLSEEPSPADCLAAQOLRNSSLIGC 101
DB 40 CVRANELCAEBSNCSRRYTLRQCLAGDRNTMLANKE-----CQALEVYQESPLYLC 93
OY 102 MCHRRKNVACLDITYVYH-----RA 123
DB 94 RCKRGKKELCLOIQTWYSIHGLTGESEFEASPEPYTSRLSDIFRLASIFSGTQDPA 153
OY 124 RSLDSDICLKFMLTLNDKGRILRAYEAS-----CPHOAHVCLROLTFPEKAAE 178
DB 154 VSTKSNHCDIAAKAANLNDNCKNLSSYSISGNREISPTERNRRKCHALNOFFDRVPS 213
OY 179 PHAQILLPCAPNDRCGGERRRNTIAPNCA--PVAPPCLELRILCFSDPCRSRLYDF 237
DB 214 EYTYMLPLCSC--DQACAEERRRQITLPSCSYEDKEKPCLDRLSCRDHLCRSRLADF 271
OY 238 QTHCP--MDLIGTCATEQSRCLRAYILGIGTAMPNPNVSNVNTSVALS--CTCRGSGNL 293
DB 272 HANCAASYRTITSCPADYQACIGSYAGIGFDMTPNVDNPTGIYVSPWCNCRGSGNM 331
OY 294 QEECEMLGFFSHNCPCLTEATPA 316
DB 332 EEECEKFLRDLFTENCLRNAIOA 354

RESULT 6
OY 015316 PRELIMINARY; PRT; 464 AA.
AC 015316:
DT 01-JAN-1998 (TRENDELREL 05, Created)
DT 01-JAN-1998 (TRENDELREL 05, Last sequence update)
DT 01-AUG-1998 (TRENDELREL 07, Last annotation update)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR BETA.
GN GDNFR-BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETAL BRAIN;
RA MARTINOVARA K., SUVANTO P., HORELLI-KUTINEN N., LINDAHL M.,
RA MOSHNAKOV M., AIRAKSINEN M.S., PALOTIE A., SARIOLA H., SAARMA M.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93703; AAB61922.1;
SQ SEQUENCE 464 AA; 51530 MW; DE80D543 CRC32;

Query Match
Best Local Similarity 25.2%; Score 509; DB 4; Length 464;
Matches 111; Conservative 44; Mismatches 113; Indels 58; Gaps 8;

OY 44 CQARRKCOADPTCSAAVYHLDSCTS--SISTPLSEEPSPADCLAAQOLRNSSLIGC 101
DB 40 CVRANELCAEBSNCSRRYTLRQCLAGDRNTMLANKE-----CQALEVYQESPLYLC 93
OY 102 MCHRRKNVACLDITYVYHAR----- 125
DB 94 RCKRGKKELCLOIQTWYSIHGLTGESEFEASPEPYTSRLSDIFRLASIFSGTADPV 153

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QY 125 -SLDSDCLCFAMCTINDKCDRLKAYGACS-----GPHCORHVCRLQLLTFEKKAAE 178
 DB 154 VSANSHCHLDAACACNLNDCKLRSSYSICNREISPTERRCKRCHALROFEDRVPS 213
 QY 179 PHAGGLICPCAPNDRCGGERRRNTIAPNCAL-PPVAPNCLERLRCFSPPLCRSLVD 237
 DB 214 EYTRMLFCSC--QODACARERROTILPSCSYDEKERNCLDLRGVCRDHLCRSLADF 271
 QY 238 QTRCHP--MDILGTCATEOSRCLRAYLGLGTANTPNEFVNNTSVALS--CTCRSGN 293
 DB 272 HANCRASTYQVTSQPDANQACISGYSAGMGFMTPTVYDSSFTGLVSVWCSCRSNGM 331
 QY 294 QEECEMLEGFFSHNPCLTEAIAA 316
 DB 332 EEECEKFLRDTFENPCIRNAIOA 354

RESULT 7
 015328 PRELIMINARY: PRT; 464 AA.

015328; 01-JAN-1998 (TREMREL. 05, Created)
 DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
 DT 01-NOV-1998 (TREMREL. 08, Last annotation update)
 DE RET LIGAND 2.
 GN RETL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 97322356.
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.,
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 DR EMBL: U97145; AAC51647.1;
 SQ SEQUENCE 464 AA; 51543 MW; 288A8BD8 CRC32;

Query Match 25.2%; Score 509; DB 4; Length 464;
 Best Local Similarity 34.4%; Pred. No. 7.4e-44;
 Matches 111; Conservative 41; Mismatches 113; Indels 58; Gaps 8;

QY 44 CLOARKCADPTCSAAYHLDSCIS--SISTPLSEPSVPADCLAAOOLNSSLIGC 101
 DB 40 CVANFELCAESNCSSRYRTLROCLAGRDRTMLANKE-----COALEVLOESPLYDC 93
 QY 102 MCHRRKNOVACLDIYTVYHAR----- 125
 DB 94 RCKRGKRLQLOIYNSHGLTEGEFEYASPEYPTSRLSDIFRLASITSGADPV 153
 QY 125 -SLDSDCLCFAMCTINDKCDRLKAYGACS-----GPHCORHVCRLQLLTFEKKAAE 178
 DB 154 VSANSHCHLDAACACNLNDCKLRSSYSICNREISPTERRCKRCHALROFEDRVPS 213
 QY 179 PHAGGLICPCAPNDRCGGERRRNTIAPNCAL-PPVAPNCLERLRCFSPPLCRSLVD 237
 DB 214 EYTRMLFCSC--QODACARERROTILPSCSYDEKERNCLDLRGVCRDHLCRSLADF 271
 QY 238 QTRCHP--MDILGTCATEOSRCLRAYLGLGTANTPNEFVNNTSVALS--CTCRSGN 293
 DB 272 HANCRASTYQVTSQPDANQACISGYSAGMGFMTPTVYDSSFTGLVSVWCSCRSNGM 331
 QY 294 QEECEMLEGFFSHNPCLTEAIAA 316
 DB 332 EEECEKFLRDTFENPCIRNAIOA 354

RESULT 8

015507 ID 015507 PRELIMINARY: PRT; 460 AA.
 AC 015507;
 DT 01-JAN-1998 (TREMREL. 05, Created)
 DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
 DT 01-NOV-1998 (TREMREL. 08, Last annotation update)
 DE RET LIGAND 1.
 GN RETL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE: 97322356.
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.,
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE: 97322356.
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.,
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SUBSTANTIA NIGRA;
 RA HISHIKI T., KONDOH K., ICHIMITA S., NIMURA Y., SEKI N., OZAKI T.,
 RA SAKIYAMA S., TAKAHASHI H., OHNUMA N., TANABE M., FUJIMURA S.,
 RA NAKAGAWARA A.,
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U97144; AAC51646.1;
 DR EMBL: U95847; AAB71811.1;
 SQ SEQUENCE 460 AA; 50838 MW; 022FEBCA CRC32;

Query Match 24.1%; Score 488; DB 4; Length 460;
 Best Local Similarity 34.7%; Pred. No. 1e-41;
 Matches 121; Conservative 42; Mismatches 122; Indels 64; Gaps 11;

QY 17 LLLPLPFLPLAA-----GDLPTESRLMNSCLQARRCQADPTCSAAYHLDSCIS-- 70
 DB 6 LFALPLDLILLSAEVSGDRL-----DCVXASDCLKEOSCSTYRTLROCVAKKE 57
 QY 70 ---SISTPLSEPSVPADCLAAOOLNSSLIGCMCHRRKNOVACLDIYTVYHAR--- 124
 DB 58 TNSLSAGLEAKD-----ECSRAMEALNOKSLYNCRCRKGKKEKNCRLITVSMYQSLQ 112
 QY 124 -----SLDSDCLCFAMCTINDKCDRLKAYGEA 154
 DB 113 NDLEDSEYEPVNSRLSDIFRVVPFISVEHHPKNNCLDAKACNLDDICKKYSATITP 172
 QY 155 C---SGPHCORHVCRLQLLTFEKKAAEPHAGGLICPCAPNDRCGGERRRNTIAPNCAL 210
 DB 173 CTSVSDVYCNRRCKRCHALROFEDRVPAKHSYGMLFCSC--RDIACTERRRQITVPCVS 230
 QY 211 PP-VAPNCLERLRCFSPPLCRSLVDQTRCHMD-ILGTCATEQ-SRCLRAYLGLGT 267
 DB 231 EEREKPNCLNQDSCKTYIKRSLADFTVQCQPSRSVSSCLLENVADCLAYSLIGT 290
 QY 268 AMTNEFVNNTSVALSCTCRSGNLOEECEMLEGFFSHNPCLTEAIAA 316
 DB 291 VMTPTVYDSSLSVAPMCDSCNSGNDLEECLEKLFNFRDNTCLNNAIOA 339

RESULT 9
 035252 ID 035252 PRELIMINARY: PRT; 463 AA.
 AC 035252;

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DR 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE GDNF RECEPTOR BETA.
GN GDNFR-BETA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57.
RA DEY B.K., WONG Y.W., TOO H.P.;
RL NeuroReport 9:0-0(0001).
[2]
RC STRAIN-C57;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
EMBL: AF015172; AAB86600.1;
SEQUENCE 463 AA; 51134 MW; 910EF17F CRC32;

Query Match          24.1%; Score 487; DB 11; Length 463;
Best Local Similarity 34.5%; Pred. No. 1.3e-41;
Matches 120; Conservative 44; Mismatches 122; Indels 62; Gaps 11;

QY 14 VLMLLLPPSPPLAAGDPLPTESRLMNSCLARRKQADPTCSAAYHHLDSTS---- 70
DB 9 VLPLDLMLMA--EVSGDRL-----DCVKASDQCLKQSCSTKRTLRQCVAKET 58
QY 70 --SISPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRMKNQVACLDIYTVHRA---- 124
DB 59 NFSITSGLEAKD-----ECSSAMEALKOKSLYNCRCKRGMKEKNCILRTYSMTQSLQGN 113
QY 124 -----RSLSDSL-----CLKFMALCTLNDKCDRLKRAYGEAC 155
DB 114 DLLEDSPYEPVNSRLSDIFRAVPFISVEHISKGNCLDAKACNLDDTCCKYRSAYITPC 173
QY 156 ----SGPHCOHVCRLQRLTFEKEAEPHAGLLCPGAPNDGCGERRRTIAPNCALP 211
DB 174 TTSMSNVCCRRCKHAKLROFEDKVPKHSYGLMFCSC--RDVACTERRRQTIYVPCSYE 231
QY 212 P-VAPNCLRLRCLFSDPLCRSLVDFQTHCHPMD-ILGTCAEQ--SRCLRAYLGLGTA 268
DB 232 ERRRPCLNLDQSCCKTYICRSRLADFTNCOPEBSRSVSCLEKNYADCLLAYSGLGTV 291
269 MTEWYSNVNTSVALSCTCRGSGNLQECCEMLGFEFSHPCLTEALTA 316
292 MPNYIDSSLSVAPMCDGCSGNDLEDCLKFNFEDNTCLKNALTA 339

RESULT 10
O43912 PRELIMINARY; PRT; 465 AA.
AC 043912;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DE 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE GFI-LINKED ANCHOR PROTEIN.
GN GFI-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA ANGIST M., JING S., BOIK S., BENTLEY K., MALLASAMY S., HALUSHKA M.,
RC FOX G.M., CHARAVARTI A.;
RL Genomics 0:0-0(1998).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE-MEDULLARY THYROID CARCINOMA TUMOR;
RA SHEPHERDINE S.E., KHORANA S., SCHULTZ P.N., HUANG E., THORE N.,
HU Z.J., FOX G.M., JING S., COTE G.J., GAGEL R.F.;

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RL Hum. Genet. 0:0-0(1998).
DR EMBL: AF038420; AAC39693.1;
DR EMBL: AF038411; AAC39693.1; JOINED.
DR EMBL: AF038412; AAC39693.1; JOINED.
DR EMBL: AF038413; AAC39693.1; JOINED.
DR EMBL: AF038414; AAC39693.1; JOINED.
DR EMBL: AF038415; AAC39693.1; JOINED.
DR EMBL: AF038416; AAC39693.1; JOINED.
DR EMBL: AF038417; AAC39693.1; JOINED.
DR EMBL: AF038418; AAC39693.1; JOINED.
DR EMBL: AF038419; AAC39693.1; JOINED.
DR EMBL: AF042080; AAB97271.1;
DR EMBL: AF038421; AAC39692.1;
DR EMBL: AF058990; AAC14431.1;
DR EMBL: AF058991; AAC14431.1; JOINED.
DR EMBL: AF058992; AAC14431.1; JOINED.
DR EMBL: AF058993; AAC14431.1; JOINED.
DR EMBL: AF058994; AAC14431.1; JOINED.
DR EMBL: AF058995; AAC14431.1; JOINED.
DR EMBL: AF058996; AAC14431.1; JOINED.
DR EMBL: AF058997; AAC14431.1; JOINED.
DR EMBL: AF058998; AAC14431.1; JOINED.
SQ SEQUENCE 465 AA; 51455 MW; 1C4EAE03 CRC32;

Query Match          24.0%; Score 485.5; DB 4; Length 465;
Best Local Similarity 34.2%; Pred. No. 1.8e-41;
Matches 121; Conservative 42; Mismatches 122; Indels 69; Gaps 11;

QY 17 LLLLLPPSPPLA-----GDPLPTESRLMNSCLARRKQADPTCSAAYHHLDSTS---- 70
DB 6 LYPALPLDLILLSAEVSGDRL-----DCVKASDQCLKQSCSTKRTLRQCVAKGE 57
QY 70 --SISPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRMKNQVACLDIYTVHRA---- 124
DB 58 TNSLSASGLEAKD-----ECSSAMEALKOKSLYNCRCKRGMKEKNCILRTYSMTQSLQGN 112
QY 124 -----RSLSDSL-----CLKFMALCTLNDKCDRLKRAYGEAC 149
DB 113 NDLEDSPYEPVNSRLSDIFRAVPFISDVFOVEHLPKGNCLDAKACNLDDTCCKYRS 172
QY 150 AYDEAC----SGPHCOHVCRLQRLTFEKEAEPHAGLLCPGAPNDGCGERRRTIAP 205
DB 173 AYTPCTGSNDVCCRRCKHAKLROFEDKVPKHSYGLMFCSC--RDVACTERRRQTIY 230
QY 206 PNCALP-VAPNCLRLRCLFSDPLCRSLVDFQTHCHPMD-ILGTCAEQ--SRCLRAYL 262
DB 231 PVCSYERRKPNCLNLDQSCCKTYICRSRLADFTNCOPEBSRSVSCLEKNYADCLLAYS 290
263 GLIGTAMTPNYSNVNTSVALSCTCRGSGNLQECCEMLGFEFSHPCLTEALTA 316
291 GLIGTAMTPNYSNVNTSVALSCTCRGSGNLQECCEMLGFEFSHPCLTEALTA 344

RESULT 11
O35246 PRELIMINARY; PRT; 468 AA.
AC 035246;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-JAN-1998 (TREMblrel. 05, Last annotation update)
DE GDNF RECEPTOR ALPHA.
GN GDNFR-ALPHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57; TISSUE-LIVER;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL NeuroReport 9:0-0(0001).
[2]

```

RP SEQUENCE FROM N.A.
RC STRAIN=C57; TISSUE=LIVER;
RA DEY B.R.; MONG Y.W.; TOO H.P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF041117; AAB86599.1;
SQ SEQUENCE 468 AA; 51751 MW; AFDCEB61 CRC32;

Query Match 24.0%; Score 485.5; DB 11; Length 468;
Best Local Similarity 34.3%; Pred. No. 1.8e-41;
Matches 121; Conservative 42; Mismatches 123; Indels 67; Gaps 11;

QY 14 VLMILLIPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAVHHLDSCTS--- 70
DB 9 VLPLDILMSA--EYSGGDR-----DCVKASDQCLKSGSTKRTLRQCVAGRET 58
QY 70 --SISTPLSEPSVPACDLAQAOLRNSSLIGCMCHRMKNVACDIYTVHRA--- 122
DB 59 NPSLISGLEAKD---ECRSAMELKKOKSLYNCRCKMKEKNCILTIYSMYSLOGN 113
QY 122 -----RARSLSDL-----CLKFAMLCTLNDKCDRLRKA 150
DB 114 DLDESPYEPVNSRLSDIFRAVPFISDVFQVEHISKGNKLDLAKACNLDLDTCKKTRSA 173
QY 151 YGEAC---SGPHCRHVCLRLQLTFEERKAEPPHAGLLCPCAPNDGCGERRRNTIAP 206
DB 174 YITPCTTSMSENEVCNRKCHRALQOFEDKVPKAKSYGMLFCSC--RDVACTERRQTIIP 231
QY 207 NCALPP-VAPNCLRLRLCFSDPLCRSLVDFQTHCHMD-ILGTCAE0-SRCLRAYLG 263
DB 232 VCSIEEREPNCLNDQSCRTNYCSRSLADFENCOPESSVSNCLEKNADCLLAYSG 291
QY 264 LIGTAMPNPNVNTSVASCTCRSGNLOECEMELEGGFSHNPCLTEAIA 316
DB 292 LIGVTMPNPNYIDSSLSVAAPWDCSNGNDEDLKPLNFKDNTCLKNIAO 344

RESULT 12

035748 PRELIMINARY; PRT; 463 AA.

AC 035748;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE GNFR-ALPHA/TRN1-DELTA PROTEIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
[1]
SEQUENCE FROM N.A.
RC STRAIN=HANNOVER;
RA ZHONG J.; ANNIES M.; HEUMANN R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ002072; CA005171.1;
SQ SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;

Query Match 24.0%; Score 485; DB 11; Length 463;
Best Local Similarity 34.4%; Pred. No. 2e-41;
Matches 120; Conservative 42; Mismatches 123; Indels 64; Gaps 11;

QY 17 LLLPLPSPPLA---GDPLPTESRLMNSCLQARRKQADPTCSAAVHHLDSCTS--- 70
DB 6 LYFALPLDILMSAEVSGGDR-----DCVKASDQCLKSGSTKRTLRQCVAGRE 57
QY 70 --SISTPLSEPSVPACDLAQAOLRNSSLIGCMCHRMKNVACDIYTVHRA--- 124
DB 58 TNSLISGLEAKD---ECRSAMELKKOKSLYNCRCKMKEKNCILTIYSMYSLOG 112
QY 124 -----RSLDSL-----CLKFAMLCTLNDKCDRLRKA 154
DB 113 NDLEDSPEYEPVNSRLSDIFRAVPFISVETISKGNKLDLAKACNLDLDTCKKTRSAITTP 172

QY 155 C---SGPHCRHVCLRLQLTFEERKAEPPHAGLLCPCAPNDGCGERRRNTIAPCAL 210
DB 173 CTSMSNEVCNRKCHRALQOFEDKVPKAKSYGMLFCSC--RIACTERRQTIIPVCSY 230
QY 211 PP-VAPNCLRLRLCFSDPLCRSLVDFQTHCHMD-ILGTCAE0-SRCLRAYLG 267
DB 231 EEREPNCLSLQSCRTNYCSRSLADFENCOPESSVSNCLEKNADCLLAYSG 290
QY 268 AMPNPNVNTSVASCTCRSGNLOECEMELEGGFSHNPCLTEAIA 316
DB 291 VMPNPNYIDSSLSVAAPWDCSNGNDEDLKPLNFKDNTCLKNIAO 339

RESULT 13

093512 PRELIMINARY; PRT; 431 AA.

AC 093512;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DE GPR RECEPTOR ALPHA 4 PRECURSOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98313402.
RA THOMPSON J.; DOXATIS E.; PINON L.G.; STRACHAN P.; BUI-BELLO A.;
RA WYATT S.; BUCHANAN V.L.; DAVIES A.M.;
RT "GFRalpha-4, a new GDNF family receptor".
RL Mol. Cell. Neurosci. 11:117-126(1998).
DR EMBL: AF045162; AAC36464.1;
KM Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 431 GPR RECEPTOR ALPHA 4.
SQ SEQUENCE 431 AA; 47964 MW; 7AE1F0B0 CRC32;

Query Match 23.2%; Score 470; DB 13; Length 431;
Best Local Similarity 33.3%; Pred. No. 6.3e-40;
Matches 105; Conservative 32; Mismatches 132; Indels 46; Gaps 8;

QY 44 CLQARRKQADPTCSAAVHHLDSCTSISIPLSEPSVPACDLAQAOLRNSSLIGCMC 103
DB 26 CLQAGSCTNDPLCCSSKEFKRLKOCIA--GNGANKLPDAKNOCRSTVTALLSQLGCKC 83
QY 104 HRPMKNVACLDIYTVHRA-----RSLD-----SD 129
DB 84 KRGMKEKHCISYVSIHHTLMGMNVLSSEPYEPFIRGDIYRLASITAGSENEYTOVN 143
QY 130 LCLKFAMLCTLNDKCDRLRKA 184
DB 144 RCLDAKACNVEMCCQLRTEYVSCIRRLARADTCNRKCHRALKFFDVPPEYTHET 203
QY 185 LCPAPNDGCGERRRNTIAPCAL-PPVAPNCLRLRLCFSDPLCRSLVDFQTHCHP 243
DB 204 LKPC--EDTACAEKRRQTIIPACSTESKEKFWCLAPLDSRENTYCRVAEFCNCP 261
QY 244 -MDILGTCAE0-SRCLRAYLGIGTAMPNPNVNTSVASCTCRSGNLOECEMELE 301
DB 262 SLQTAGCRSDSYAACLLAYTGIIIGSPIIPNIDNTSSIAFQCTONAGNQBCESTL 321
QY 302 GFSHNPCLTEAIA 316
DB 322 HLFEDNVCLQNALIAO 336

RESULT 14

0922A3 PRELIMINARY; PRT; 358 AA.

AC 0922A3;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 1999, 20:17:04 : Search time 27.76 seconds

(without alignments)
1508.874 Million cell updates/sec

Title: US-09-272-835-20

Perfect score: 4675

Sequence: 1 MGSTARLGAIVLFTVIVGL.....DASLRKADPNRFRCKDLPVL 888

Scoring table: BLOSUM62

arched: 142080 seqs, 47169319 residues

PIR-62: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2403	51.4	890	1	A53743	protein-tyrosine k
2	2399	51.3	882	2	I38912	receptor tyrosine
3	2337.5	50.0	723	2	I38412	receptor tyrosine
4	2257	48.3	880	1	JC4166	protein-tyrosine k
5	2246	48.0	880	2	B53743	protein-tyrosine k
6	2246	48.0	876	2	I49152	protein-tyrosine k
7	2080	44.5	856	2	I58411	protein-tyrosine k
8	1880	40.2	397	2	JE0082	GPI-linked recepto
9	1204.5	25.8	894	1	A4157	protein-tyrosine k
10	1178.5	25.2	888	2	S23065	ufo protein - mous
11	1155.5	24.7	999	2	I38547	novel cellular pro
12	1137	24.3	994	2	I49276	c-mer tyrosine kin
13	1130.5	24.2	942	2	S23251	protein-tyrosine k
14	1102.5	23.6	974	1	A49714	protein-tyrosine k
15	1061.5	22.7	442	1	B43362	protein-tyrosine k
16	811	17.3	600	2	A56379	protein-tyrosine k
17	696	14.9	1369	1	JC4860	env-sea polyprotel
18	662.5	14.2	596	1	TVFVSA	protein-tyrosine k
19	658.5	14.1	1404	1	A48196	protein-tyrosine k
20	645.5	13.8	1378	1	I48751	protein-tyrosine k
21	615.5	13.2	1379	1	S01254	hepatocyte growth
22	613	13.1	1375	1	JC5148	hepatocyte growth
23	612.5	13.1	1367	1	IGHUR1	hepatocyte growth
24	610	13.0	2554	1	TVF7L	kinase-related pro
25	609.5	13.0	640	2	S23008	insulin-like growt
26	606	13.0	1380	1	TVHUME	insulin-like growt
27	600	12.8	1400	1	I38185	hepatocyte growth
28	596	12.7	1371	2	A33837	insulin-like growt
29	590.5	12.6	1115	1	S29926	protein-tyrosine k
30	587	12.6	2594	2	A53774	protein-tyrosine k
31	586.5	12.5	1382	1	INHR	kinase-related pro
32	585	12.5	1580	1	TVFRA	insulin receptor p
33	583	12.5	1899	2	I38153	gene retill protein
34	583.5	12.4	1372	2	A34157	insulin receptor p
35	579.5	12.3	1064	1	S57450	insulin receptor p
36	576.5	12.3	1383	2	A36080	insulin receptor p
37	574.5	12.3	1114	1	S05882	protein-tyrosine k
38	573.5	12.3	1300	2	A36502	insulin receptor-t
39	570.5	12.2	981	1	FOHWGM	gag-abl polyprotel

40	569	12.2	1123	2	A39962	kinase-related tra
41	568.5	12.2	402	1	TVFYUR	protein-tyrosine k
42	568	12.1	801	4	TVHURE	transforming prote
43	566.5	12.1	402	2	B34735	protein-tyrosine k
44	566	12.1	477	2	JN0291	protein-tyrosine k
45	565.5	12.1	873	2	S60740	protein-tyrosine k

ALIGNMENTS

RESULT 1
A53743
protein-tyrosine kinase (EC 2.7.1.112) tyros precursor - human
N:Alternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase rse
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A53743; J0077; J02145; S32765; S32219
R:Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Goddard, A.; Godowski, P.J.
J. Biol. Chem. 269, 10720-10728, 1994
A>Title: rse, a novel receptor-type tyrosine kinase with homology to Axl/Ufo, is expr
A:Reference number: A53743; M01D:94193774
A:Accession: A53743
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-890 <NA>
A:Cross-references: GB:U05682; NID:9463469; PIDN:AAA19236.1; PID:9463470
R:Onasli, K.; Mizuno, K.; Kuma, R.; Miyata, T.; Nakamura, T.
Oncogene 9, 699-705, 1994
A>Title: Cloning of the cDNA for a novel receptor tyrosine kinase, Sky, predominantly
A:Reference number: J00777; M01D:94150991
A:Accession: J00777
A:Molecule type: mRNA
A:Residues: 1-890 <NA>
A:Cross-references: DDBJ:D17517; NID:9624880; PIDN:BAA04467.1; PID:d1004992; PID:9624
A:Experimental source: hepatoma Hep3 cell
R:Polvi, A.; Armstrong, E.; Lai, C.; Lemke, G.; Huebner, K.; Spritz, R.A.; Gulda, L.C
Gene 114, 289-293, 1993
A>Title: The human TYRO3 gene and pseudogene are located in chromosome 15q14-q25.
A:Reference number: J02145; M01D:94085793
A:Accession: J02145
A:Molecule type: mRNA
A:Residues: 519-790 <POL>
A:Cross-references: EMBL:X72886; NID:9286020; PIDN:CAA51396.1; PID:g312336
R:Polvi, A.; Armstrong, E.; Lai, C.; Lemke, G.; Huebner, K.; Spritz, R.A.; Gulda, L.C
Submitted to the EMBL Data Library, March 1993
A:Description: Human TYRO3 gene and pseudogene in chromosome 15pter-q25.
A:Reference number: S32765
A:Accession: S32765
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 519-790 <POL>
A:Cross-references: EMBL:X72886; NID:9286020; PIDN:CAA51396.1; PID:g312336
C:Genetics:
A:Gene: GDB:TYRO3
A:Cross-references: GDB:134764; OMIM:600341
A:Map position: 15q15.1-15q21.1
C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; imm
C:Keywords: ATP; brain; glycoprotein; growth factor receptor; phosphotransferase; tra
F:1-41/Domain: (or 7-41) signal sequence #status predicted <SIG>
F:42-990/Product: protein-tyrosine kinase tyros #status predicted <NA>
F:60-119/Domain: immunoglobulin homology <IMM>
F:156-205/Domain: immunoglobulin homology <IMM>
F:224-309/Domain: fibronectin type III repeat homology <FN3A>
F:322-405/Domain: fibronectin type III repeat homology <FN3B>
F:429-451/Domain: transmembrane #status predicted <IMM>
F:516-793/Domain: protein kinase homology <KIN>
F:524-532/Region: protein kinase ATP-binding motif
F:63,191,230,240,293,366,380/Binding site: carbohydrate (asn) (covalent) #status pred

Query Match 51.4% Score 2403; DB 1; Length 890;
Best Local Similarity 96.1%; Pred. No. 2.9e-113;

Matches 467; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

QY 382 FSDMDADSTFVVOQNSNPAMRAMVAVGLVLTALVTAALALILLRKRKRETFRGOAF 441
 DB 405 WSOPLVYVSHDRAGQGGPHSRSTSMVPPVGLVLTALVTAALALILLRKRKRETFRGOAF 464
 QY 442 DSVARGEPAVHFRAARSFNRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 501
 DB 465 DSVARGEPAVHFRAARSFNRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 524
 QY 502 GKGEFGSVREAOIKQEDGSEFVAVKMLKADIIASDIEEFLREAACKEDPHVAKLV 561
 DB 525 GKGEFGSVREAOIKQEDGSEFVAVKMLKADIIASDIEEFLREAACKEDPHVAKLV 584
 QY 562 GVSLSRAKGRPLIPVYILPFMKHGDHLAFLASRIGENFNPLOTILRFVWDIACGME 621
 DB 585 GVSLSRAKGRPLIPVYILPFMKHGDHLAFLASRIGENFNPLOTILRFVWDIACGME 644
 QY 622 YLSRNFIHDLAARNKMLAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 681
 DB 645 YLSRNFIHDLAARNKMLAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 704
 QY 682 ADNLTYVQSDVMAFGVTWMEINTRGOTPYAGIENAEIYNYLIGNRKLPQPCMEDVYDL 741
 DB 705 ADNLTYVQSDVMAFGVTWMEINTRGOTPYAGIENAEIYNYLIGNRKLPQPCMEDVYDL 764
 QY 742 MYQWMSADPKORPSTFCIRMELENILGOLSVLASODPLYINIERAEEPTAGSLELPGR 801
 DB 765 MYQWMSADPKORPSTFCIRMELENILGOLSVLASODPLYINIERAEEPTAGSLELPGR 824
 QY 802 DOPYSGADGSGMGAVGTPSDCRITLTPGGLAEPQGAHQEPSPINETORLLILLOQGL 861
 DB 825 DOPYSGADGSGMGAVGTPSDCRITLTPGGLAEPQGAHQEPSPINETORLLILLOQGL 884
 QY 862 LPHSSC 867
 DB 885 LPHSSC 890

RESULT 2
 138912
 receptor tyrosine kinase - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
 C:Accession: J38912
 R:Crossier, K.E.; Hall, L.R.; Lewis, P.M.; Morris, C.M.; Wood, C.R.; Morris, J.C.; Crossier
 Growth Factors 11, 137-144, 1994
 A:Title: Isolation and characterization of the human DTK receptor tyrosine kinase.
 A:Reference number: 138912; MUID:95161080
 A:Accession: J38912
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-882 <RES>
 A:Cross-references: EMBL:U18934; NID:9622984; PIDN:AAC50070.1; PID:9622985
 A:Genetics:
 A:Gene: DTK
 C:Superfamily: protein-tyrosine kinase ax1; fibronectin type III repeat homology; immuno
 F:508-785/Domain: protein kinase homology <KIN>

Query Match 51.3%; Score 2399; DB 2; Length 882;
 Best Local Similarity 95.9%; Pred. No. 4.5e-113;
 Matches 466; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 382 FSDMDADSTFVVOQNSNPAMRAMVAVGLVLTALVTAALALILLRKRKRETFRGOAF 441
 DB 397 WSOPLVYVSHDRAGQGGPHSRSTSMVPPVGLVLTALVTAALALILLRKRKRETFRGOAF 456
 QY 442 DSVARGEPAVHFRAARSFNRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 501
 DB 457 DSVARGEPAVHFRAARSFNRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 516
 QY 502 GKGEFGSVREAOIKQEDGSEFVAVKMLKADIIASDIEEFLREAACKEDPHVAKLV 561

DB 517 GKGEFGSVREAOIKQEDGSEFVAVKMLKADIIASDIEEFLREAACKEDPHVAKLV 576
 QY 562 GVSLSRAKGRPLIPVYILPFMKHGDHLAFLASRIGENFNPLOTILRFVWDIACGME 621
 DB 577 GVSLSRAKGRPLIPVYILPFMKHGDHLAFLASRIGENFNPLOTILRFVWDIACGME 636
 QY 622 YLSRNFIHDLAARNKMLAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 681
 DB 637 YLSRNFIHDLAARNKMLAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 696
 QY 682 ADNLTYVQSDVMAFGVTWMEINTRGOTPYAGIENAEIYNYLIGNRKLPQPCMEDVYDL 741
 DB 697 ADNLTYVQSDVMAFGVTWMEINTRGOTPYAGIENAEIYNYLIGNRKLPQPCMEDVYDL 756
 QY 742 MYQWMSADPKORPSTFCIRMELENILGOLSVLASODPLYINIERAEEPTAGSLELPGR 801
 DB 757 MYQWMSADPKORPSTFCIRMELENILGOLSVLASODPLYINIERAEEPTAGSLELPGR 816
 QY 802 DOPYSGADGSGMGAVGTPSDCRITLTPGGLAEPQGAHQEPSPINETORLLILLOQGL 861
 DB 817 DOPYSGADGSGMGAVGTPSDCRITLTPGGLAEPQGAHQEPSPINETORLLILLOQGL 876
 QY 862 LPHSSC 867
 DB 877 LPHSSC 882

RESULT 3
 138412
 receptor tyrosine kinase - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
 C:Accession: J38412
 R:Del, W.; Pan, H.; Gupta, S.L.; Murphy, M.J.
 Oncogene 9, 975-979, 1994
 A:Title: Molecular cloning of a novel receptor tyrosine kinase, tlf, highly expressed
 A:Reference number: 138412; MUID:94151024
 A:Accession: J38412
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-723 <RES>
 A:Cross-references: EMBL:U02566; NID:9467817; PIDN:AAA17407.1; PID:9467818
 C:Superfamily: protein-tyrosine kinase ax1; fibronectin type III repeat homology; imm
 F:331-606/Domain: protein kinase homology <KIN>

Query Match 50.0%; Score 2337.5; DB 2; Length 723;
 Best Local Similarity 92.9%; Pred. No. 4.4e-110;
 Matches 461; Conservative 7; Mismatches 25; Indels 3; Gaps 3;

QY 382 FSDMDADSTFVVOQNSNPAMRAMVAVGLVLTALVTAALALILLRKRKRETFRGOAF 441
 DB 220 WSOPLVYVSHDRAGQGGPHSRSTSMVPPVGLVLTALVTAALALILLRKRKRETFRGOAF 279
 QY 442 DSVARGEPAVHFRAARSFNRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 501
 DB 280 DSVARGEPAVHFRAARSFNRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 339
 QY 502 GKGEFGSVREAOIKQEDGSEFVAVKMLKADIIASDIEEFLREAACKEDPHVAKLV 561
 DB 340 GKGEFGSVREAOIKQEDGSEFVAVKMLKADIIASDIEEFLREAACKEDPHVAKLV 399
 QY 562 GVSLSRAKGRPLIPVYILPFMKHGDHLAFLASRIGENFNPLOTILRFVWDIACGME 621
 DB 400 GVSLSRAKGRPLIPVYILPFMKHGDHLAFLASRIGENFNPLOTILRFVWDIACGME 458
 QY 622 YLSRNFIHDLAARNKMLAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 681
 DB 459 YLSRNFIHDLAARNKMLAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 518
 QY 682 ADNLTYVQSDVMAFGVTWMEINTRGOTPYAGIENAEIYNYLIGNRKLPQPCMEDVYDL 741

Db 519 ADNLTYQSDVMAFGVTWMEIMTRGQTPYAGIENAEIYNLLIGN-LKQPECMEDVYL 577

QY 742 MYOCMSADPKORPSFTCLRMLEENILGOLSVLASODPLYINIERAEPTAGSGLELPGR 801

Db 578 MYOCMSADPKORPSFTCLRMLEENILGOLSVLASODPLYINIERAEPTAGSGLELPGR 637

QY 802 DQRYSGAGDGGSGMGAVGTPSDCRYILTPGGIAPQPOAEHQEPSPLENTORLLLOOGL 861

Db 638 DQRYSGAGDGGSGMGAVGTPSDCRYILTPGGIAPQPOAEHQEPSPLENTORLLLOOGL 697

QY 862 LPHSSCADSLKMAKP 877

Db 698 L-HTVAVSPOERASGP 712

RESULT 4

JC4166

protein-tyrosine kinase (EC 2.7.1.112) tyros3 precursor - rat

Alternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase rse

Species: Rattus norvegicus (Norway rat)

Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: J04166; P0185

R:Ohashi, K.; Honda, S.; Ichinomiyu, N.; Nakamura, T.; Mizuno, K.

J. Biochem. 117, 1267-1275, 1995

F:Title: Molecular cloning and in situ localization in the brain of rat sky receptor ty

A:Reference number: JC4166; MUID:96104999

A:Molecule type: mRNA

A:Residues: 1-880 <OH>

A:Cross-references: DBJ:D37880; NID:91498195; PIDN:BA07119.1; PID:d1007696; PID:g82905

A:Experimental source: brain

A>Note: It is uncertain whether Met-1 or Met-7 is the initiator

R:Lat, C.; Lemke, G.

Neuron 6, 691-704, 1991

F:Title: An extended family of protein-tyrosine kinase genes differentially expressed in

A:Reference number: P0185; MUID:91222560

A:Accession: P0185

A:Molecule type: mRNA

A:Residues: 650-703 <LA1>

A:Experimental source: sciatic nerve

C:Comment: This receptor plays an important role in development, function, and maintain

C:Genetics:

A:Gene: tyro-3

C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; immun

C:Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transforming

F:1-31/Domains: (or 7-31) signal sequence #status Predicted <SIG>

F:32-880/Product: (or 32-874) protein-tyrosine kinase tyros3 #status predicted <MAT>

0-109/Domains: immunoglobulin homology <IMM1>

F:146-195/Domains: immunoglobulin homology <IMM2>

F:214-299/Domains: fibronectin type III repeat homology <FN3A>

F:312-395/Domains: fibronectin type III repeat homology <FN3B>

F:419-441/Domains: transmembrane #status predicted <TM>

F:506-783/Domains: protein kinase homology <KIN>

F:514-522/Region: protein kinase ATP-binding motif

F:515-766/Domains: cytoplasmic tyrosine kinase #status predicted <CTK>

F:533,75,181,220,230,283,356,370/Binding site: carbohydrate (Aan) (covalent) #status pred

Query Match 48.3%; Score 2257; DB 1; Length 880;

Best Local Similarity 90.3%; Pred. No. 5,7e-106;

Matches 439; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 382 FSQDADSTFVSVOOQNSPAMRAMVPIVGLTALYMAAALILILKRRKRETFGQAF 441

Db 395 MSQPLVSSHHDAGQGPPHSTSWPVVGLTALYMAAALILILKRRKRETFGQAF 454

QY 442 DSVARGPAPVAFRAARSPFRERPERIENTLDSIGISDELKRELDVILPEQOFTLGRML 501

Db 455 DSVARGPAPVAFRAARSPFRERPERIENTLDSIGISDELKRELDVILPEQOFTLGRML 514

QY 502 GKGGGSGVREAOIKREDGSFVKVAVKMLKADIIASSDIEEFLREAAKKEFDHPVAKLV 561

Db 515 GKGGGSGVREAOIKREDGSFVKVAVKMLKADIIASSDIEEFLREAAKKEFDHPVAKLV 574

QY 562 GVALRSRAKRLPIPVILIPFKHGDILHAFLLASRIGENPFNLPOTLIRFWDIACGNE 621

Db 575 GVALRSRAKRLPIPVILIPFKHGDILHAFLLASRIGENPFNLPOTLIRFWDIACGNE 634

QY 622 YLSRNFIHDLAARNCMAEDTVCVADPGLSRKITYSDYRQGCASLPRKMLALESL 681

Db 635 YLSRNFIHDLAARNCMAEDTVCVADPGLSRKITYSDYRQGCASLPRKMLALESL 694

QY 682 ADNLTYQSDVMAFGVTWMEIMTRGQTPYAGIENAEIYNLLIGNRLKQPECMEDVYL 741

Db 695 ADNLTYQSDVMAFGVTWMEIMTRGQTPYAGIENAEIYNLLIGNRLKQPECMEDVYL 754

QY 742 MYOCMSADPKORPSFTCLRMLEENILGOLSVLASODPLYINIERAEPTAGSGLELPGR 801

Db 755 MYOCMSADPKORPSFTCLRMLEENILGOLSVLASODPLYINIERAGPQAEHNSPELPG 814

QY 802 DQRYSGAGDGGSGMGAVGTPSDCRYILTPGGIAPQPOAEHQEPSPLENTORLLLOOGL 861

Db 815 DQRYSGAGDGGSGMGAVGTPSDCRYILTPGGIAPQPOAEHQEPSPLENTORLLLOOGL 874

QY 862 LPHSSC 867

Db 875 LPHSSC 880

RESULT 5

B53743

protein-tyrosine kinase (EC 2.7.1.112) tyros3 precursor - mouse

N:Alternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase rse; ty

C:Species: Mus musculus (house mouse)

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999

C:Accession: B53743; S44141; J02146; I49198; I49151; I48863; I48860

R:Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Goddard, A.; Godowski, P.J.

J. Biol. Chem. 269, 10720-10728, 1994

F:Title: rse, a novel receptor-type tyrosine kinase with homology to Axl/Vfo, is expr

A:Reference number: A53743; MUID:94193774

A:Accession: B53743

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-880 <MA>

A:Cross-references: GB:U05683; NID:9469518; PIDN:AAA19237.1; PID:g469519

R:Lat, C.; Gore, M.; Lemke, G.

Submitted to the EMBL Data Library, March 1994

A:Description: Structure, expression and activity of TYRO3.

A:Reference number: S44141

A:Accession: S44141

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 7-629, 'R', 631-810, 'V', 812-880 <LA1>

A:Cross-references: EMBL:X78103; NID:9473096; PIDN:CAA54995.1; PID:g473097

R:Polvi, A.; Armstrong, E.; Lat, C.; Lemke, G.; Huebner, K.; Spitt, R.A.; Gulde, L.C

Gene 134, 289-293, 1993

F:Title: The human TYRO3 gene and pseudogene are located in chromosome 15q14-q25.

A:Reference number: J02146; MUID:94085793

A:Accession: J02146

A:Molecule type: mRNA

A:Residues: 509-629, 'R', 631-647, 'P', 649-780 <POL>

R:Crozier, P.S.; Lewis, P.M.; Hall, L.R.; Vltas, M.R.; Morris, C.M.; Beler, D.R.; Woo

Growth Factors 11, 125-136, 1994

F:Title: Isolation of a receptor tyrosine kinase (DTK) from embryonic stem cells: str

A:Reference number: I49198; MUID:95161079

A:Accession: I49198

A:Status: Preliminary

A:Molecule type: translated from GB/EMBL/DBDB

A:Residues: 1-880 <RES>

A:Cross-references: EMBL:U18933; NID:9622982; PIDN:AAC52148.1; PID:g622983

R:Schulz, N.T.; Pauliac, C.I.; Lee, L.; Zhou, R.

Brain Res. Mol. Brain Res. 28, 273-280, 1995

F:Title: Isolation and expression analysis of tyros3, a murine growth factor receptor

A:Reference number: I49151; MUID:95240399

A:Accession: I49151

A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBDB

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A:Molecule type: mRNA
A:Residues: 7-880 <RE2>
A:Cross-references: EMBL:U18342; NID:9687625; PIDN:AA826942.1; PID:9687626
R:Blieschke, L.G.; Gianola, D.M.; Emerson, S.G.
Oncogene 10, 2239-2242, 1995
A:Title: Identification of alternative exons, including a novel exon, in the tyrosine kinase
A:Reference number: 148861; MUID:95503487
A:Accession: 148863
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-92 <RE3>
A:Cross-references: EMBL:U23721; NID:9901992; PIDN:AAC52217.1; PID:9901996
R:Rial, C.; Gore, M.; Lemke, G.
Oncogene 9, 2567-2578, 1994
A:Title: Structure, expression, and activity of Tyro 3, a neutral adhesion-related receptor
A:Reference number: 148860; MUID:94336210
A:Accession: 148860
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 7-629, 'R', 631-810, 'V', 812-880 <RE4>
Oss-references: EMBL:X78103; NID:9473096; PIDN:CAA54995.1; PID:9473097
A:Gene: tyro3; Dtk: Etk2/tyro3
A:Introns: 32/1
C:Superfamily: glycin-tyrosine kinase ax1; fibronectin type III repeat homology; Immunoglobulin
C:Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transforming
F:1-31/Domian: (or 7-31) signal sequence #status predicted <SIG>
F:32-880/Product: protein tyrosine kinase tyro3 #status predicted <MAT>
F:50-109/Domian: immunoglobulin homology <IMM2>
F:146-195/Domian: immunoglobulin homology <IMM2>
F:214-299/Domian: fibronectin type III repeat homology <FN3A>
F:312-395/Domian: fibronectin type III repeat homology <FN3B>
F:419-441/Domian: transmembrane #status predicted <TM>
F:506-783/Domian: protein kinase homology <KIN>
F:514-532/Region: protein kinase ATP-binding motif
F:515-766/Domian: cytoplasmic tyrosine kinase #status predicted <CTR>
F:53,75,181,220,230,283,356,370/Binding site: carbohydrate (asn) (covalent) #status predicted
Query Match 48.0%; Score 2246; DB 2; Length 880;
Best Local Similarity 90.1%; Pred. No. 2e-105;
Matches 438; Conservative 14; Mismatches 34; Indels 0; Gaps 0;
QY 382. FSGQADSTFSVQOQNSNPNRANVPVYGLVALVTAAALAILLKKRRKTRFGQAF 441
DB 395 WSQPLVSSHSHAGQSPHRTSWPVYGLVALVTAAALAILLKKRRKTRFGQAF 454
QY 442 DSVARGPAYHFRARSEFNREPRIRATIDSGISSELKEKEDVLIPEOQTTLGRL 501
DB 455 DSVARGPAYHFRARSEFNREPRIRATIDSGISSELKEKEDVLIPEOQTTLGRL 514
QY 502 GKEGFSVREAOIKQEDSFYKVAVKMLADIIASSDIEELFRAACKEEDHFAVKLV 561
DB 515 GKEGFSVREAOIKQEDSFYKVAVKMLADIIASSDIEELFRAACKEEDHFAVKLV 574
QY 562 GVSLSRAKRGALPIPVYLIPTPKHGDLHAFTLASRIGENPNPLQGLIVRMVDIAGME 621
DB 575 GVSLSRAKRGALPIPVYLIPTPKHGDLHAFTLASRIGENPNPLQGLIVRMVDIAGME 634
QY 622 YLSSNFIHRLAARNCLAEADMTVCVADFEGLSKRIISGDIYRGGCAKSLPYKTLAEST 681
DB 635 YLSSNFIHRLAARNCLAEADMTVCVADFEGLSKRIISGDIYRGGCAKSLPYKTLAEST 694
QY 682 ADNLYTVOSDVMAEGLTMEITRGQTPYAGIENAEIYNYLIGNRKAKOPECEDEYDL 741
DB 695 ADNLYTVHSDVMAEGLTMEITRGQTPYAGIENAEIYNYLIGNRKAKOPECEDEYDL 754
QY 742 MYQCSADPKRQPEFTCLRMLENILGQLSVLSASQDPLYINIERAEPTAGSGLELPGR 801
DB 755 MYQCSADPKRQPEFTCLRMLENILGQLSVLSASQDPLYINIERAEPTAGSGLELPGR 814
QY 802 DQPSGAGDSGGMGVGSTPDCRYLLTPGGLAPQDAHQHPSPINERQILLIQGL 861
DB 814 DQPSGAGDSGGMGVGSTPDCRYLLTPGGLAPQDAHQHPSPINERQILLIQGL 861

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QY	862	LPHSSC	867	
Db	875	LPHSSC	880	
RESULT 6				
	149152	protein-tyrosine kinase (EC 2.7.1.112) tyro3, isoform B - mouse		
		N:alternate names: tyrosine kinase growth factor receptor		
		C:Species: Mus musculus (house mouse)		
		C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999		
		C:Accession: I49152, I48861		
		R:Schulz, N.T.; Paulhac, C.I.; Lee, L.; Zhou, R.		
		Brain Res. MOL. Brain Res. 28, 273-280, 1995		
		A:Title: Isolation and expression analysis of tyro3, a murine growth factor receptor		
		A:Reference number: I49151; MUID:95240399		
		A:Accession: I49152		
		A:Status: preliminary; translated from GB/EMBL/DBJ		
		A:Molecule type: mRNA		
		A:Residues: 1-876 <RES>		
		A:Cross-references: EMBL:U03343; NID:9687627; PIDN:AA26943.1; PID:9687628		
		R:Biesecker, L.G.; Giamola, D.M.; Emerson, S.G.		
		Oncogene 10, 2239-2242, 1995		
		A:Title: Identification of alternative exons, including a novel exon, in the tyrosine		
		A:Reference number: I48861; MUID:95303487		
		A:Accession: I48861		
		A:Status: preliminary; translated from GB/EMBL/DBJ		
		A:Molecule type: DNA		
		A:Residues: 1-88 <RES>		
		A:Cross-references: EMBL:U23721; NID:9901992; PIDN:AC52215.1; PID:9901994		
		C:Genetics:		
		A:Gene: tyro3; Etk2/tyro3		
		A:Introns: 28/1		
		C:Superfamily: protein-tyrosine kinase axl, fibronectin type III repeat homology; Imm		
		C:Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase		
		F:43-105/Domain: Immunoglobulin homology <IM>		
		F:502-779/Domain: protein kinase homology <KM>		
		F:510-518/Region: protein kinase ATP-binding motif		
QY	382	FSQMDADSTFVVOONSNP	48.08; Score 2246; DB 2; Length 876;	
Db	391	WSQPLVSSHHAGRCQPPHRSRTSMVPVGLVLTALITAAALAILKRRKRETFQAF	Best Local Similarity 90.18; Pred. No. 2e-105;	
			Matches 438; Conservative 14; Mismatches 34; Indels 0; Gaps 0;	
QY	442	DSVARGEPAVHFRANSFNRPERPERIEATLDSIGISDELKEKLEVDLIEQOFTLRML		
Db	451	DSVARGEPAVHFRANSFNRPERPERIEATLDSIGISDELKEKLEVDLIEQOFTLRML		
QY	502	GKGGGSGREOLQOEQSGFYKVAVKMLKADITASSSIEFLRLRAACMKEDPHRAKLV		
Db	511	GKGGGSGREOLQOEQSGFYKVAVKMLKADITASSSIEFLRLRAACMKEDPHRAKLV		
QY	562	GVSLSRAKGLPIPIVILPFRKGGDLHAFLLASRIENFNPILQTLVFNMDIACGM		
Db	571	GVSLSRAKGLPIPIVILPFRKGGDLHAFLLASRIENFNPILQTLVFNMDIACGM		
QY	622	YLSSRNITRHDLLAARNCMLEDMTVCVADFGSLSKITVSGDYRQGCASKLPVKMLAEST		
Db	631	YLSSRNITRHDLLAARNCMLEDMTVCVADFGSLSKITVSGDYRQGCASKLPVKMLAEST		
QY	682	ADNLTYYTQSDVMAAGVYVMEIMTNGOTFYAGIEAEATYNTLIGNRLKOPPECMEDVYDL		
Db	691	ADNLTYYTQSDVMAAGVYVMEIMTNGOTFYAGIEAEATYNTLIGNRLKOPPECMEDVYDL		
QY	742	MYQWMSADPKQORSFTCLRAELENTIGQLSVLSAODPLVINTIERAEPTAGSLLEPGR		
Db	751	MYQWMSADPKQORSFTCLRAELENTIGQLSVLSAODPLVINTIERAEPTAGSLLEPGR		

QY 802 DOPYSGADGSGMVGSTPSPDCRYILPGGLAEQPGAEHPESPPLNWTQRLLLQGL 861
 Db 811 ERSSSEADGSGVAGVIGIPSDSRITFPGGLSESPGLEQPEPLNENRLLQGL 870
 QY 862 LPHSSC 867
 Db 871 LPHSSC 876

RESULT 7

158411
 protein-tyrosine kinase (EC 2.7.1.112) birt - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 18-Jun-1999
 C:Accession: 158411
 R:Fujimoto, J.; Yamamoto, T.
 Oncogene 9, 693-698, 1994.
 .Title: birt, a mouse gene encoding a novel receptor-type protein-tyrosine kinase, is pr
 Reference number: 158411; MUID:94150990
 .Accession: 158411

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-856 <RES>
 A:Cross-references: GB:D17393; NID:9801867; PID:BA04216.1; PID:9801868
 C:Superfamily: protein-tyrosine kinase xtl; fibronectin type III repeat homology; immun
 C:Keywords: ATP; glycoprotein; phosphotransferase
 F:501-778/Domain: protein kinase homology <Kin>
 F:509-511/Region: protein kinase ATP-binding motif

Query Match 44.5%; Score 2080; DB 2; Length 856;
 Best Local Similarity 87.7%; Pred. No. 3.9e-97;
 Matches 408; Conservative 15; Mismatches 40; Indels 2; Gaps 1;

QY 382 FSQDWDSTFVVOQNSNPAMRAVPEVGLTALVTAALAILLRKRKRERFGQAF 441
 Db 390 WSPPLVYSSHDHNGRQCPHSRSTSVVYGLTALITAAALILLRKRKRERFGQAF 449
 QY 442 DSWMAGEPAVHRAARSENREPERLEATLDSIGISDELKEKLEDEVLIEQOFTLGRML 501
 Db 450 DSWMAGEPAVHRAARSENREPERLEATLDSIGISDELKEKLEDEVLIEQOFTLGRML 509
 QY 502 GKEEFSVRAQAKQEGSGSVKAYAKLADITASSDIEEFLRAACMEFDPHVAKL 561
 Db 510 GKEEFSVRAQAKQEGSGSVKAYAKLADITASSDIEEFLRAACMEFDPHVAKL 569
 QY 562 GVALRSRAKRLPIPMYILPFMKHGDHAFLLASRIGENFNPLOTLLRPMVDIAGME 621
 Db 570 GVALRSRAKRLPIPMYILPFMKHGDHAFLLASRIGENFNPLOTLLRPMVDIAGME 629
 QY 622 YLSSRNFIHDLAARNCMAEDMTVCVADFLSRKITSGDYRQGCASKLPYKWLAESE 681
 Db 630 YLSSRNFIHDLAARNCMAEDMTVCVADFLSRKITSGDYRQGCASKLPYKWLAESE 689
 QY 682 ADNLTVQVSVYAFVGTMTMIRGCTPPVAGINAEIYNTLIGNRLKOPPECEMEDYDL 741
 Db 690 ADNLTVQVSVYAFVGTMTMIRGCTPPVAGINAEIYNTLIGNRLKOPPECEMEDYDL 749
 QY 742 MYOCWADPQKRSFYCLRLLENILGOLSVLASODPLINIERKEEPNAGSLPEGR 801
 Db 750 MYOCWADPQKRSFYCLRLLENILGOLSVLASODPLINIERKEEPNAGSLPEGR 809
 QY 802 DOPYSGADGSGMVGSTPSPDCRYILTPGGL--ADPGQAEHP 844
 Db 810 ERSSSEADGSGVAGVIGIPSDSRITFPGGLAEQPGAEHP 854

RESULT 8
 JE0082
 GPI-linked receptor precursor - mouse
 N:Alternate names: GFRalpha-3
 C:Species: Mus musculus (house mouse)

C>Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 17-Mar-1999
 C:Accession: JE0082
 R:Nomoto, S.; Ito, S.; Yang, L.X.; Kitch, K.
 Biochem. Biophys. Res. Commun. 244, 849-853, 1998
 A:Title: Molecular cloning and expression analysis of GFRalpha-3, a novel cDNA related
 A:Reference number: JE0082; MUID:98205811

A:Accession: JE0082
 A:Molecule type: mRNA
 A:Residues: 1-397 <NOM>
 A:Cross-references: DDBJ:AB008833; NID:92627159; PID:92627160
 C:Comment: This protein plays a distinct role in cell survival and differentiation.
 C:Keywords: glycoprotein
 F:1-25/Domain: signal sequence
 F:380-397/Region: hydrophobic
 F:92,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.2%; Score 1880; DB 2; Length 397;
 Best Local Similarity 94.1%; Pred. No. 1.8e-87;
 Matches 354; Conservative 5; Mismatches 11; Indels 6; Gaps 1;

QY 54 LEAGNSLATENREYNSTQTKRRCANPACAKAYOHLGCTSSLSRPLLESAMADCL 113
 Db 25 LGAGNSLATENREYNSTQTKRRCANPACAKAYOHLGCTSSLSRPLLESAMADCL 84
 QY 114 EAAEOLANSLIDCRHRKHOATCIDITWTVHPARSLGDELDVSPYEDPTSKPMK 173
 Db 85 EAAEOLANSLIDCRHRKHOATCIDITWTVHPARSLGDELDVSPYEDPTSKPMK 144
 QY 174 NLSKLNKLPDSDLCFAMLCITLHDKCDRLKRAYGEAGSGIRCOHILCAQLRSFEK 233
 Db 145 NLSKLNKLPDSDLCFAMLCITLHDKCDRLKRAYGEAGSGIRCOHILCAQLRSFEK 204
 QY 234 AESHAQGLICPPPPDAGGERRNTIAPSCALPSVTNCLDLRSFCRADPLCRSLMD 293
 Db 205 AESHAQGLICPPPPDAGGERRNTIAPSCALPSVTNCLDLRSFCRADPLCRSLMD 264
 QY 294 FQTHCHPMDLIGTCATGOSRCLRAYLGLTANTPFISKVNTVYALSTCGSGSLMD 353
 Db 265 FQTHCHPMDLIGTCATGOSRCLRAYLGLTANTPFISKVNTVYALSTCGSGSLMD 324
 QY 354 CEOLERSFQNPCLVPAIAAKMFRHQLFSQDWDSTFVVOQNSNPALR-----LQ 413
 Db 325 CEOLERSFQNPCLVPAIAAKMFRHQLFSQDWDSTFVVOQNSNPALR-----LQ 378
 QY 414 LFLVYRAALALILR 429
 Db 379 LFLVYRAALALILR 394

RESULT 9

158411
 protein-tyrosine kinase (EC 2.7.1.112) axl precursor, major splice form - human
 N:Alternate names: transforming protein axl; UFO receptor
 C:Species: Homo sapiens (man)
 C>Date: 28-May-1992 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
 C:Accession: A41527; B38269; J39203; G02782
 R:O'Bryan, J.P.; Fyfe, R.A.; Cogswell, P.C.; Neuberger, A.; Kitch, B.; Prokop, C.; Esp
 Mol. Cell. Biol. 11, 5016-5031, 1991
 A:Title: axl, a transforming gene isolated from primary human myeloid leukemia cells,
 A:Reference number: A41527; MUID:92017777
 A:Accession: A41527
 A:Molecule type: mRNA
 A:Residues: 1-884 <OAB>
 A:Cross-references: GB:M76125
 A:Experimental source: axl(+)
 A:Accession: B41527
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-337, 'K', 339-428, 438-894 <OAB>
 A:Cross-references: GB:M76125; NID:9292869; PID:AAA61243.1; PID:9292870
 A:Experimental source: axl(-)
 A>Note: the authors translated the codon AAG for residue 338 as Leu

R:Partanen, J.; Maekela, T.P.; Allitalo, R.; Lehtvaestaho, H.; Allitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A:Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A:Reference number: A38268; M0ID:91062389
A:Accession: B38269
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 674-730 <PAR>
A:Cross-references: GB:M59373; GB:M37781
R:Schulz, A.S.; Schleithoff, L.; Faust, M.; Barttram, C.R.; Janssen, J.W.
Oncogene 8, 509-518, 1993
A:Title: The genomic structure of the human UFO receptor.
A:Reference number: I39203; M0ID:93149614
A:Accession: I39203
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <SCH>
A:Cross-references: EMBL:X66030; NID:g37594; PIDN:CAA46829.1; PID:g37595
R:Mitchell, P.J.
Submitted to the EMBL Data Library, December 1990
Reference number: G09377
Accession: G07782
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-302, 'P', 304-429, 'E', 431-638, 'G', 640-894 <MIT>
A:Cross-references: EMBL:X57019; NID:g37592; PIDN:CAA40338.1; PID:g37593
C:Comment: This protein is overexpressed in chronic myelogenous leukemia and induces nec
C:Genetics:
A:Gene: GDB:AXL, UFO
A:Cross-references: GDB:I33764; OMIM:109135
A:Map position: 19q13.1-19q13.1
C:Function:
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; immun
C:Keywords: alternative splicing; ATP; duplication; glycoprotein; leukemia; magnesium; p
tein kinase
F:1-32/Domain: signal sequence <status predicted <SIG>
F:33-894/Product: protein-tyrosine kinase axl, major splice form <status predicted <AXJ>
F:49-119/Domain: immunoglobulin homology <IM1>
F:153-207/Domain: immunoglobulin homology <IM2>
F:224-320/Domain: fibronectin type III repeat homology <FN3A>
F:333-411/Domain: fibronectin type III repeat homology <FN3B>
F:448-472/Domain: transmembrane <status predicted <TM>
F:543-810/Domain: protein kinase homology <KIN>
F:542-550/Region: protein kinase ATP-binding motif
F:43,157,199,339,345,401/Binding site: carboxylate (Asn) (covalent) <status predicted
F:567,586,672/Active site: Lys, Glu, Asp <status predicted
F:703/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) <status pred
/79,821/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) <status pred

Query Match 25.8%; Score 1204.5; DB 1; Length 894;
Best Local Similarity 51.1%; Pred. No. 2.4e-53;
Matches 243; Conservative 73; Mismatches 131; Indels 29; Gaps 9;

386 WADSTFVYQ---QNSNA--WRAMPVYVGLTALYTAALAILLKRKRKTRFGQA 440
426 WPPGQAQPHQLVKKEPSPAFSPWMT-VLGAAYAAACVLLALFLVHRKRKTRFGYEV 484
441 EDSVARGEPAYHFAASFNREPERIEATLDSIGISDELKEDLVLPDQOFTLRM 500
485 PEPYEREGELVYRKYRSYSR---RTTEATLNSIGISEELKEDLVWDRHKAALGKT 541
501 LKGEFSGVREAOIKQEDGSFYKAVKMLKADIIASSDIEFLREAAKKEFDHPHVKL 560
542 LEEGFEFVMEGOLNODD-SILKVAIVKTKIAICTRSELEDFLSAYCKMEKDEHNVRL 600
561 VGVSLRSKAKGLPIPMILPMMKGDIAFLASRIGENPNPLQTLIRFMDIACGM 620
601 IGVCGSSESEFPAVVPILPMMKGDHSLFLYSLRGLDQVPTLPTOMLVFMADIAGM 660
621 EYLSRNFIHRDLAARNCLMADMTVCVADFGLSRKITYSGDYRGGASKLPVKKLALES 680

661 EYLSRNFIHRDLAARNCLMENNMSVADFGLSRKITYSGDYRGGASKLPVKKLALES 720
681 LADNLYTQSDYVAFVATMEITRGOTPYAGIENAEYTNLIGNRKKOPECKEDYVD 740
721 LADRYTSSKSDVMSGVATMEIATNGOTPYEVSELYTDLRQGNRKLQPDGGLYA 780
741 LMYQWSDAPKORPSFTGLRMELENILGOLSVLSADPLYNIERA---EETPAGSL 796
781 LMSRCMEINPQORPSFTGLRMELENILGOLSVLSADPLYNIERA---EETPAGSL 840
797 ELPGDQYSGAGDSGGANGGTPSDCRITLTPG-----GLAEPGQAE 841
841 DPTQPDKDC---SCLTAEVHPAG-RYVLCPESTPSPAPADRGSPAPAGORD 892

RESULT 10
S23065
ufo protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 01-Sep-1995 #text_change 16-Jul-1999
C:Accession: S23065
R:Faust, M.; Ebensperger, C.; Schulz, A.S.; Schleithoff, L.; Hamelster, H.; Barttram,
Oncogene 7, 1287-1293, 1992
A:Title: The murine ufo receptor: molecular cloning, chromosomal localization and in
A:Reference number: S23065; M0ID:92319537
A:Accession: S23065
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-888 <FNU>
A:Cross-references: EMBL:X63535; NID:g55121; PIDN:CAA45097.1; PID:g55122
C:Genetics:
A:Gene: ufo
C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; imm
C:Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F:43-113/Domain: immunoglobulin homology <IM1>
F:528-804/Domain: protein kinase homology <KIN>
F:536-544/Region: protein kinase ATP-binding motif

Query Match 25.2%; Score 1178.5; DB 2; Length 888;
Best Local Similarity 51.3%; Pred. No. 4.7e-52;
Matches 237; Conservative 69; Mismatches 129; Indels 27; Gaps 6;

399 SNPAMRA---WBPVYVGLTALYTAALAILLKRKRKTRFGQAEDSVARGEPAYH 454
433 SEPPRAFSPWMTVYVGLAAYAAACVLLALFLVHRKRKTRFGYEVPEPYERELVYR 492
455 RAANSFNREPERIEATLDSIGISDELKEDLVLPDQOFTLRMKGEGSVREAOI 514
493 RYRKSYSR---RTTEATLNSIGISEELKEDLVWDRHKAALGKTIGEFGFVMEGOL 549
515 KQEGSPYKAVVVKMLKADIIASSDIEFLREAAKKEFDHPHVKLVGSLRSKAKGLP 574
550 NQDD-SILKVAIVKTKIAICTRSELEDFLSAYCKMEKDEHNVRLIGYCGQSDREGFP 608
575 IPAVILPMMKGDIAFLASRIGENPNPLQTLIRFMDIACGMLEYLSRNFIHRDLA 634
609 EPVYILPMMKGDHSLFLYSLRGLDQVPTLPTOMLVFMADIAGMELYSKRIRHDLA 668
635 ARNCLMADMTVCVADFGLSRKITYSGDYRGGASKLPVKKLALESADNLYTQSDYVA 694
669 ARNCLMENNMSVADFGLSRKITYSGDYRGGASKLPVKKLALESADNLYTQSDYVA 728
695 FGVATMEITRGOTPYAGIENAEYTNLIGNRKKOPECKEDYVDLMYQWSDAPKORP 754
729 FGVATMEIATNGOTPYEVSELYTDLRQGNRKLQPDGGLYSMSRCMEINPQORP 788
755 SFTCLRMELENILGOLSVLSADPLYNIERA---EETPAGSLPGRDQYSGAGD 810
789 SFARLDRLENTLALPAPDEILVNMDEGSHLEPGAGAGADPTQPPD---KD 844
811 GSGGANGGTPSDCRITLTPG-----GLAEPGQAE 841

Db 845 SCSCLTADVSHAGRYVLCPTAGPTLADRCPCAPFGED 886

RESULT 11

138547

novel cellular proto-oncogene - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999

C:Accession: 138547

R:Graham, D.K.; Dawson, T.L.; Mullaney, D.L.; Snodgrass, H.R.; Earp, H.S.

Cell Growth Differ. 5, 647-657, 1994

A:Title: Cloning and mRNA expression analysis of a novel human protooncogene, c-mer.

A:Reference number: 138547; MUID:94368701

A:Accession: 138547

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-999 <GRA>

A:Cross-references: EMBL:U08023; NID:9505664; PIDN:AAB60430.1; PID:9505665

Genetics:

Gene: c-mer

C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; Immunc

F:585-861/Domain: protein kinase homology <KIN>

Query Match 24.7%; Score 1155.5; DB 2; Length 999;

Best Local Similarity 38.8%; Pred. No. 7.4e-51;

Matches 294; Conservative 115; Mismatches 20; Indels 141; Gaps 27;

233 AAESH-----AGCLL-----CPCPEDAGCGERRNTAPSCALPSV-----TP--N 273

Db 261 SCEAHNDKGLTVSOQVOINRAIPSPTEVSI-----RNSTASHILISWVGDFGSPFRN 316

QY 274 C-LDLRSCRADPLCRSLMDPQCHCHMDLIGTCATQSSRLRAY-----LGILG-TA 325

Db 317 CSTGVK---EADPLONGVMYFNTSALP---HLQIKOLQALANYSIGVSCMNDIGMSA 369

QY 326 MTP-----NFISKYNTVAL-----SCTCGSS 347

Db 370 VSPWILASTEGASVAVLANLTVFLNBSNDVNDIMKPRPYQDQGVYRISHWQSA 429

QY 348 GNLODECEQLERFSQ-----NPLVEALIAAKRPHROLFS-----QDMAD-S 389

Db 430 GISKELEEVQONGSFRARISYOVHNATCTVLAATRGVGFSPVKEIFPAHWQYA 489

QY 390 TFSVYQOONSPPARAWPVVLG-----VLTALVTAALALILKRKRKEFGQAF--- 442

Db 490 PSSIPADGNADP-----VLIFGCGFGFILGLILYISLA---IKRVOETKFGNAFTEE 541

QY 442 DSVARAGEPAVHFAARAFNRPERRERIPATLDSIGISDELKEDVLIIPDQFTLGRL 501

Db 542 DS-----ELVYNYIAKSKFCR---RAILELTHLSAGVSELDQKEDVDYIDNLLILGIL 593

QY 502 GKGFSGYREAOQLKOEDGSFYKAVKMLKADIIASSDIEELREAAKKEEDHPHYATLY 561

Db 594 GEGFSGYMEENLKOEDGTSIKVAVKTKLDSNSHREIEELSEAAKCKDPSHPVITLL 653

QY 562 GVSLSRAKGRLPDPVITLPKKGDLAAFLAARIGENPNPLQTIIRMVADIACME 621

Db 654 GVCLEMSQG-TPKAPVILPPTKGTDLTYLLYSRLTETGPKHPIQLTKPMVDIALGME 712

QY 622 YLSRNFIRHDLAARNCMLAEDMTVCVADFGLSRRIYSGDYRROGCAKSLPVKMLALESL 681

Db 713 YLSRNFIRHDLAARNCMLAEDMTVCVADFGLSRRIYSGDYRROGCAKSLPVKMLALESL 772

QY 682 ADNTLYVQSVAFVAGVTMMELTRGQTPYAGIENAEIYNYLIGNRKLQPECKMEDVDL 741

Db 773 ADRTYTSKSDYMAFGVTMMELTRGQTPYAGIENAEIYNYLIGNRKLQPECKMEDVDL 832

QY 742 MYOQWASDPKQRPFTCLRLMEENILGOLSTLSASQDPLYN---IERAEPTLGGSL-E 797

Db 833 MTSCHWTDPLDRPTFSVLRQLLEKLESLDVRNQADVITYNTOLLESSEGLAOGPTLAP 892

QY 798 LPGRDQPYSGAGDGSQMGAVG-----GRPSDCKYLLTRGSC-----LAEPGAQEHQ 844

Db 893 LDNLNDPDSITINCTPPRAISVYVAEVDHDSKPHREGRIYILNGSSEMEDLTSAPSAATVAE 952

QY 845 ESSLNETORLL-----LIQGLLPSSCADASLKMAD 876

Db 953 KNSVLPGERLYANGVSWSHSSMLPLGSSLPDELLFAD 989

RESULT 12

149276

c-mer tyrosine kinase receptor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999

C:Accession: 149276

R:Graham, D.K.; Bowman, G.W.; Dawson, T.L.; Stanford, W.L.; Earp, H.S.; Snodgrass, H.

Oncogene 10, 2349-2359, 1995

A:Title: Cloning and developmental expression analysis of the murine c-mer tyrosine k

A:Reference number: 149276; MUID:95303502

A:Accession: 149276

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-994 <RES>

A:Cross-references: EMBL:U21301; NID:9885969; PIDN:AAA80222.1; PID:9885970

C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; Imm

C:Keywords: ATP; receptor

F:580-856/Domain: protein kinase homology <KIN>

F:588-596/Region: protein kinase ATP-binding motif

Query Match 24.3%; Score 1137; DB 2; Length 994;

Best Local Similarity 53.2%; Pred. No. 6.2e-50;

Matches 236; Conservative 71; Mismatches 103; Indels 34; Gaps 10;

QY 409 VVLG-----VLTALVTAALALILKRKRKEFGQAF---DSVYAGEPVHFAARAF 460

Db 499 IILGFCGFIILIGLILCISLA---LRRVQETKFGAFSEDSOL-----VNYRAKSKF 550

QY 461 NRPERRIEATLDSIGISDELKEDVLIIPDQFTLGRLMKGCFSGYREAOQLKOEDGS 520

Db 551 CR---RAIELTQSLGVSEELQNKEDVDYIDNLLYGVKLVGESEFSGVMEGNLKOEDGT 607

QY 521 FVYAVYKMLKADIIASSDIEELREAAKKEEDHPHYAKLVGSLSRKANGRLDPVYL 580

Db 608 SOKYAVYKMLKDNFSOREIEELSEAAKMDFNHPYIRLGVCIELSSQG-IPKPVYL 666

QY 581 PFMKHGDPAFLASRIGENPNPLQTIIRMVADIACMEYSSRNFIRHDLAARNCML 640

Db 667 PFMKGTDLHTLILSRNLNTGPKYIHLOTLLKFMMDIAGMEYLSNRFIRHDLAARNCML 726

QY 641 AEDMTVCVADFGLSRRIYSGDYRROGCAKSLPVKMLALESLADNLVYVQSVAFVAGVTM 700

Db 727 RDMTVCVADFGLSKRIYSGDYRROGRIAKMPYKMAIESEADRVYTSKSDYMAFGVTM 766

QY 701 EIMRGQTPPAGINATYNYLIGNRLKQPECKMEDVDYLMATQCSADKQRPSTCLR 760

Db 787 EITRGMTPTPGVQNHMEYLYLLGHRLKQPECKMEDVDYIMKSCWADPLDRPTFSVLR 846

QY 761 MELFNILGOLSTLSASQDPLYNIERAE--EPTAGSLELPGRD---QPSAGDGSQMG 815

Db 847 LQLEKLESPLDADKRSITTYINTQLLESCEGIANLP-SLTGLMDNIDPDSITIACTPGA 905

QY 816 AVGTGTPSDC-----RYILTPG 831

Db 906 AVSVYTALEVHNNLRERYILNGG 929

RESULT 13

523251

protein-tyrosine kinase (EC 2.7.1.112) ark precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 19-Dec-1997

C:Accession: 523251

R:Rescigno, J.; Mansukhani, A.; Basilio, C.
 Oncogene 6, 1909-1913, 1991
 A:Title: A putative receptor tyrosine kinase with unique structural topology.
 A:Reference number: S23251, MID:92019811
 A:Accession: S23251
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-942 <RES>
 A:Cross-references: EMBL:X59560
 C:Genetics:
 A:Gene: ark
 C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; immunoglobulin; ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
 F:1-19/Domain: signal sequence; status predicted <Sig>
 F:20-942/Product: protein-tyrosine kinase ark status predicted <Kat>
 F:446-466/Domain: transmembrane status predicted <TM>
 F:528-804/Domain: protein kinase homology <KIN>
 F:536-544/Region: protein kinase ATP-binding motif
 F:151,192,339,395,677/Binding site: carbohydrate (Asn) (covalent) status predicted

Query Match 24.2% Score 1130.5; DB 2; Length 942;
 Best Local Similarity 57.4%; Pred. No. 1.2e-49;
 Matches 220; Conservative 62; Mismatches 92; Indels 9; Gaps 4;

QY 399 SNPAMRA---WPPVYGVLTALVTAALALILRRRRKRRFGAOFDSVMAAGEPAVHP 454
 DB 433 SEPPPAFSPWYVYVLLGALVAAACVILALFLVHRKRTKRGVEEPVEPELVARI 492
 QY 455 RAARSRNRRPERIEATLDSIGISDELKEKEDVLIPEOQFTGRMGKEFGSVRAEOL 514
 DB 493 RVKRSYSR---RTTEATLNSLIGISEELKEKRLDVMVDNRHVALMGKLGSEGEAVNEGDL 549
 QY 515 KODSGFVVAVMKADITIASDIEEFLREAAKMEFDPHVAIKVGLSRKRAKGRIP 574
 DB 550 NODD-SILVAAYTKIVICTRSELEDFSEAVCKMEFHPNVMRIKGYCFQSGSDREGPP 608
 QY 575 IPWVILPFMKHGDIAFLASRIGENPFLPLOTILRFWDVINGMEYLSRRHTRDIA 634
 DB 609 EPPVILPFMKHGDIAFLASRIGENPFLPLOTILRFWDVINGMEYLSRRHTRDIA 668
 QY 635 ARNCMLAEDMTVCVADFGLSRKITYSGDYRQGCASRLPVKWLAEADLNTVVSQDVA 694
 DB 669 ARNCMLNENNSVCVADFGLSRKITYSGDYRQGCASRLPVKWLAEADLNTVVSQDVA 728
 QY 695 FGVTMEINTRGOTPYPAJENAEIYVYLGNRLKOPPECMEDVDLMTQCSADPKORP 754
 DB 729 FGVTMEINTRGOTPYPAJENAEIYVYLGNRLKOPPECMEDVDLMTQCSADPKORP 788
 755 SFTCLMELENITIGQLSVLSAQ 777
 DB 789 SFAELREDELNTL-KICPLLRQ 810

RESULT 14
 A49714

protein-tyrosine kinase (EC 2.7.1.112) c-eyk precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A49714
 R:Jia, R.; Hanafusa, H.
 J. Biol. Chem. 269, 1839-1844, 1994
 A:Title: The proto-oncogene of v-eyk (v-ryk) is a novel receptor-type protein tyrosine kinase
 A:Reference number: A49714, MID:94124527
 A:Accession: A49714
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-974 <JIA>
 A:Cross-references: GB:L21719; MID:9438522; PIDN:AAC38010.1; PID:9438523
 C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; immunoglobulin; ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
 F:575-851/Domain: protein kinase homology <KIN>
 F:583-591/Region: protein kinase ATP-binding motif

Query Match 23.6% Score 1102.5; DB 1; Length 974;
 Best Local Similarity 48.2%; Pred. No. 3.2e-48;
 Matches 235; Conservative 75; Mismatches 141; Indels 37; Gaps 9;

QY 409 VYLGVLTALVTAALAL---ILRRRRKRRFGAOFDSVMAAGEPAVHPRAARSENR 462
 DB 494 VALGFVCGTV-AVGLILCLSVIQRCKETKYNFNRDS-----ELVYNTAKRSYCR 547
 QY 463 EPPERIEATLDSIGISDELKEKEDVLIPEOQFTGRMGKEFGSVRAEOLKODSGSV 522
 DB 548 ---RAVELLIGSLGVSSSELQKLDVINDRNLSTGLVGESEFGSVMEGRISOPEGTQ 604
 QY 523 KVAVMKADITIASDIEEFLREAAKMEFDPHVAIKVGLSRKRAKGRIPVILP 582
 DB 605 KVAAYTKMDNSHREIEEFLSEAAKMEFDPHVAIKVGLSRKRAKGRIPVILP 663
 QY 583 MKHGDIAFLASRIGENPFLPLOTILRFWDVINGMEYLSRRHTRDIAARCMLE 642
 DB 664 MKTGDSHFLSLRLEMAPOFVPLQMLKFWVDIALGMEYLSRRHTRDIAARCMLE 723
 QY 643 DMTVCVADFGLSRKITYSGDYRQGCASRLPVKWLAEADLNTVVSQDVAAGVTMMEI 702
 DB 724 DMTVCVADFGLSRKITYSGDYRQGCASRLPVKWLAEADLNTVVSQDVAAGVTMMEI 783
 QY 703 MTRGOTPYPAJENAEIYVYLGNRLKOPPECMEDVDLMTQCSADPKORPSTCLME 762
 DB 784 ATRGMPYPAJENAEIYVYLGNRLKOPPECMEDVDLMTQCSADPKORPSTCLME 843
 QY 763 LENITIGQLSVLSAQDPLXINERAE-----PTAGSLPEGRDOPYSQA 808
 DB 844 LEKLESIPAPRGSKDYVYVNTSLPEESPSTODGLDSVFPQADSDLD-PGDIAPCCS 902
 QY 809 GDSGMAVGCPSPSCRIITLPGSLAEOPGAOHEPESPLNETQILLQGLDLSHSCA 868
 DB 903 HTKALVAVDIDHSGSKYLV-----EESGPTEDAVYPLPHEGSANTESTLTPVSSSL 956
 QY 869 DASLKMAD 876
 DB 957 AAOLPCAD 964

RESULT 15
 B43362

protein-tyrosine kinase (EC 2.7.1.112) ryk - avian retrovirus RPL30
 C:Species: avian retrovirus RPL30
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Feb-1997
 C:Accession: B43362
 R:Jia, R.; Mayer, B.J.; Hanafusa, T.; Hanafusa, H.
 J. Virol. 66, 5975-5987, 1992
 A:Title: A novel oncogene, v-ryk, encoding a truncated receptor tyrosine kinase is transcribed as a env-ryk polyprotein
 A:Reference number: A43362, MID:92407992
 A:Accession: B43362
 A:Molecule type: genomic RNA
 A:Residues: 1-442 <JIA>
 A:Cross-references: GB:M92847
 A:Note: this protein is synthesized as a env-ryk polyprotein
 C:Genetics:
 A:Gene: ryk
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase;
 F:43-318/Domain: protein kinase homology <KIN>
 F:51-59/Region: protein kinase ATP-binding motif
 F:77/Active site: Lys status predicted

Query Match 22.7% Score 1061.5; DB 1; Length 442;
 Best Local Similarity 49.4%; Pred. No. 1.6e-46;
 Matches 217; Conservative 72; Mismatches 125; Indels 25; Gaps 6;

QY 452 VHPAARSRNRRPERIEATLDSIGISDELKEKEDVLIPEOQFTGRMGKEFGSVRE 511
 DB 511 VHPAARSRNRRPERIEATLDSIGISDELKEKEDVLIPEOQFTGRMGKEFGSVRE 511

```

Db      5 VNYTAKSYCR--RAVELTIGSVSSELOKQKIDVYIDRNALSLGKYLGESEGSVME 61
QY      512 AOLKQEDGSFVAVAYKMLKADIIASDIEEFLREACMEFDHPHYAKLVGSLRSRANG 571
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      62 GRLSOPEGTPOKVAVKTMKLDNFSHREIEEFLSEACIKDFHPNVIKILGVCIELSQ- 121
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      572 RLPIPMVILPEKKHGDHAFELASRIGENPFILOTILRFMYDINAGMEYLSRNFIHR 631
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121 QIPKPMVVLPEKKYDLSHLSRLEMAPQFVPLQMLKFMVDIALGMEYLSRQFLHR 180
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      632 DLARNCMIAEDMTVCVADFGLSRKIYSGDYRROCASKLPYKMLALLESADNLTYOSD 691
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      181 DLARNCMILRDMTCVADFGLSKTIYSGDYRROCRIAMFYKMLAIESLADRYTTKSD 240
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      692 VMARGVIMELTRGOTPYAGIENAEIYNYLLIGNRLKOPPECMEVDYDLMYOCWSADPK 751
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      241 VMARGVIMELTRGOTPYAGIENAEIYNYLLIGNRLKOPPECMEVDYDLMYOCWSADPK 300
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      752 QRPSTCLRMELNLTGQSVLSASQDPXYINIERAE-----PIAGSILE 797
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        301 DRPTFSQKLVHLEKLESIPAPRGSKDVIYVNTSLPEESPDSSTODIGLDSVTPQADSDLD 360
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      798 LPGRDQPYSGAGDSSGMGAVGTPSDCRYILPPGLAEQPGQAEHQEPSPLENTQRLIL 857
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      361 -PGDIAEPCCSHTRALAVVDIHGGSRIYLESEG---SPTEDAYVQPLP--HEGSANT 413
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      858 QQGLPHSSCADASIKMAD 876
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      414 EASTLPVGSLSLAQLPCAD 432
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: December 12, 1999, 20:17:12
 Job time: 1100 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:27:10 ; Search time 29.27 Seconds

(without alignments)
718,595 Million cell updates/sec

Title: US-09-272-835-20

Perfect score: 4675

Sequence: 1 MCGTAARLGAIVLVIVGL.....DASLAKMDPRFRGKDLPLV 888

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2403	51.4	890	1 R7845	Human Rse rPTK. Hu
2	2399	51.3	876	1 R60547	Human developmenta
3	2399	51.3	850	1 R60548	Mature human devel
4	2246	48.0	874	1 R60545	Murine development
5	2246	48.0	850	1 R60546	Mature murine deve
6	2239	47.9	880	1 R7846	Mouse Rse rPTK. Hu
7	2238	47.9	874	1 W79145	Receptor protein t
8	2238	47.9	874	1 W81402	Human brain-specif
9	1886.5	40.4	887	1 Y07286	Human Ret ligand R
10	1880	40.2	887	1 Y07286	Human Ret ligand R
11	1779	38.1	397	1 W37461	A GDNFR-alpha-rela
12	1658	35.5	346	1 W37465	Mouse Ret ligand R
13	1567	33.5	400	1 W37463	Human Ret ligand R
14	1567	33.5	400	1 W65116	Human GDNF alpha-3
15	1567	33.5	400	1 W65116	Human GDNF alpha-3
16	1563	33.4	400	1 W84186	Glial cell line-de
17	1561	33.4	400	1 W65117	A GDNFR-alpha-rela
18	1452	31.1	378	1 W84185	Human GDNF alpha-3
19	1341	28.7	315	1 W37462	Human Ret ligand R
20	1204.5	25.8	894	1 R85753	Human axl receptor
21	1204	25.8	885	1 R85754	Human axl receptor
22	1155.5	24.7	999	1 R87511	Human c-mer protoo
23	802	17.2	600	1 R91215	Sperm receptor kin
24	725.5	15.5	847	1 W11941	gd. trkb fusion use
25	718	15.4	814	1 W11940	gd. trkb fusion use
26	717	15.3	850	1 W11942	gd. trkb fusion use
27	682	14.6	172	1 W65118	Human GDNF alpha-3
28	621.5	13.3	489	1 W84298	Consensus sequence
29	618.5	13.2	488	1 W84183	Consensus sequence
30	612.5	13.1	1367	1 R60795	Human IFG-1. recept
31	612.5	13.1	1367	1 R91429	Human type I insul
32	612.5	13.1	1367	1 W37692	Human insulin-like
33	612.5	13.1	1367	1 W54876	Human insulin-like
34	611.5	13.1	1367	1 W54876	Human insulin-like
35	600	12.8	1400	1 R95244	IGF-1 receptor. In
36	597.5	12.8	1370	1 R91430	Human RON receptor
37	587.5	12.6	1370	1 P60005	Rat type I insulin
38	586.5	12.5	1382	1 R77440	Sequence encoded b
39	586	12.5	664	1 W71604	Wild type. human in
40	586	12.5	664	1 W71604	Rat neurturin rece
41	586	12.5	464	1 W71602	Rat neurturin rece
42	586	12.5	464	1 W84181	A GDNFR-alpha-rela
43	585.5	12.5	464	1 W92299	Rat GDNFR-beta pol
					A GDNFR-alpha-rela

ALIGNMENTS

RESULT	1	
ID	R77845	R77845 standard; protein; 890 AA.
AC	R77845;	
DT	01-NOV-1995	(first entry)
DE	Human Rse rPTK.	
KW	RSE; receptor protein tyrosine kinase; rPTK; diagnostic; therapy;	
KW	neurodegenerative disease; Alzheimer disease; Parkinson disease;	
KW	kidney disease.	
OS	Homo sapiens.	
PH	Key	
FT	peptide	Location/Qualifiers
FT	modified_site	1..40
FT	modified_site	/label= Sig_peptide
FT	modified_site	63
FT	modified_site	/label= N-glycosylation_site
FT	modified_site	191
FT	modified_site	/label= N-glycosylation_site
FT	modified_site	230
FT	modified_site	/label= N-glycosylation_site
FT	modified_site	240
FT	modified_site	/label= N-glycosylation_site
FT	modified_site	293
FT	modified_site	/label= N-glycosylation_site
FT	modified_site	366
FT	modified_site	/label= N-glycosylation_site
FT	modified_site	380
FT	modified_site	/label= N-glycosylation_site
FT	domain	429..451
FT	domain	/label= Transmembrane_domain
FT	domain	518..786
FT	domain	/label= Tyrosine_kinase_domain
FT	binding_site	525..530
FT	binding_site	/label= Mg2+-ATP_binding_site
PD	MO9514776-A.	
PD	01-JUN-1995.	
PR	15-NOV-1994.	U13214.
PR	23-NOV-1993; US-157563.	
PR	20-DEC-1993; US-170568.	
PR	05-AUG-1994; US-286305.	
PA	(GETH) GENENTECH INC.	
PA	(NEME.) NEW ENGLAND DEACONESS HOSPITAL.	
PI	Godowski PJ, Mark MR, Scadden DR, Sadick MD, Wong WLT;	
DR	WPI, 95-206933/27.	
DR	N-Psdb; Q94421.	
PT	Human and murine receptor protein tyrosine kinase(s) and corresp. DNA -	
PT	for stimulation of cell growth and differentiation e.g. for treatment of	
PT	neurodegenerative and kidney diseases	
PS	Claim 6; Fig.1A; 119P; English.	
CC	Primers based on conserved sequences from tyrosine kinases were used	
CC	to amplify fragments of tyrosine kinase encoding genes from cDNA	
CC	prepared from human brain RNA. Amplified fragments were combined,	
CC	and a composite sequence, given in Q94421, of a new receptor protein	
CC	tyrosine kinase, Rse, was determined. The extracellular domain of	
CC	RSE is useful therapeutically.	
50	Sequence 890 AA;	

Query Match	Score	DB ID	Length
Best Local Similarity	96.1%	Pred. No. 3.7e-200;	Indels 0; Gaps 0;
Matches 467; Conservative 4; Mismatches 15;			
382 FQGDADSTFFSVQOONSPPARAWPVYLVLTALYAAALALILRRRRTFRGAF	441		
405 WQGPVYVSHDRAAGQGGPHSTSNVYVGLVLTALYAAALALILRRRRTFRGAF	464		
442 DSVMAGEPAVHFRARSRFRERIRATLDSIGISDELKEDLVILPEQOFTLGRML	501		

Dd	465	D5YMAKGEPAVHAFRAASFNRERPERIATLDSIGISDELKEDVLIPEQGTJGRML	524
Qy	502	GGEFGSVAREMOLKOEODGSFYKVAVKMLKADIIASSDIEEFLREAAKKEFDHPHAKV	561
Dd	525	GKGEFGSVAREMOLKOEODGSFYKVAVKMLKADIIASSDIEEFLREAAKKEFDHPHAKV	584
Qy	562	GVSLSRAKGRPLIPMYLILPPMKAGDDHAFLAARISENPNNLPLQTLIRPMYDIACME	621
Dd	585	GVSLSRAKGRPLIPMYLILPPMKAGDDHAFLAARISENPNNLPLQTLIRPMYDIACME	644
Qy	622	YLSRNFIIHRDLAARNCMLEADMTVCYADFGLSKITYSGDYHQGCAASKIPYKMLALESL	661
Dd	645	YLSRNFIIHRDLAARNCMLEADMTVCYADFGLSKITYSGDYHQGCAASKIPYKMLALESL	704
Qy	682	ADNLYTVQSDVMAFGVTMWEIMTRGQTPYAGIENAEIYNTLIGGNRLKOPPECMEDVYDL	741
Dd	705	ADNLYTVQSDVMAFGVTMWEIMTRGQTPYAGIENAEIYNTLIGGNRLKOPPECMEDVYDL	764
Qy	742	MYQWCAADPPQRPSFTCLRLMELENILGQLSVLSASODPLYINTERAEEPTAGSSELPGR	801
Dd	765	MYQWCAADPPQRPSFTCLRLMELENILGQLSVLSASODPLYINTERAEEPTAGSSELPGR	824
Qy	802	DQYYSAGDGSAGAVGCTPSSDCRYLITRGLAEQPGAEHOPESPNTFORLLILOGL	861
Dd	825	DQYYSAGDGSAGAVGCTPSSDCRYLITRGLAEQPGAEHOPESPNTFORLLILOGL	884
Qy	862	LPHSSC	867
Dd	885	LPHSSC	890

RESULT 2
 R60547 ID R60547 standard; Protein; 876 AA.
 AC R60547;
 DT 14-APR-1995 (first entry)
 DE Human developmental tyrosine kinase (Dtk).
 KW Receptor tyrosine kinase; developmental tyrosine kinase;
 KW vertebrate development.
 OS Homo sapiens.
 PN M09419463-A.
 PD 01-SEP-1994.
 PF 16-FEB-1994; NZ0009.
 PR 16-FEB-1993; NZ-245917.
 PA (AUCK-) AUCKLAND UNISERVICES LTD.
 PI Croslier KE, Croslier PS;
 DR WPI: 94-294328/36.
 RE NP-PSDB: 071334.
 PT Developmental tyrosine kinase(s) and their ligands - used to
 PS stimulate the proliferation of cells that form part of the CNS
 PS Claim 4; Page 60-64; 86pp; English.
 CC Dtk is a transmembrane receptor tyrosine kinase whose extracellular
 CC domains contain two immunoglobulin-like motifs followed by two
 CC fibronectin-type III repeats. It is distinguished from RTKs having
 CC the equivalently structured extracellular domains by its potential
 CC function based upon its distribution within the mammalian body. (RTK
 CC - receptor tyrosine kinase).
 SQ Sequence 876 AA;

Query Match	51.3%	Score 2399;	DB 1;	Length 876;
Best Local Similarity	95.9%	Pred. No. 86-200;		
Matches 466;	Conservative 4;	Mismatches 16;	Indels 0;	Gaps 0;

[illegible]

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0Y 502 GGERGSVEAEALKEKEDGSEFVKVAVKMLKADIIASSDIEEFLREAAKCKEEDHPVAKLV 561
Db 511 GGERGSVEAEALKEKEDGSEFVKVAVKMLKADIIASSDIEEFLREAAKCKEEDHPVAKLV 570
0Y 562 GVSLSRAKGRPIPMVILTPMKHGDHAEFLARIGENPNLPLQTLIRFMDIACME 621
Db 571 GVSLSRAKGRPIPMVILTPMKHGDHAEFLARIGENPNLPLQTLIRFMDIACME 630
0Y 622 YLSNNEFTHRDIAANCMIAEDMTVCVADEGLSRKITYSGDYRGGCASKIPYMWLLESL 681
Db 631 YLSNNEFTHRDIAANCMIAEDMTVCVADEGLSRKITYSGDYRGGCASKIPYMWLLESL 690
0Y 682 ADNLTVOSDVMWAGVYMWELMTFGQTPVAGIENAEIYNYLIGGNRLKOPPECMEDVYDL 741
Db 691 ADNLTVOSDVMWAGVYMWELMTFGQTPVAGIENAEIYNYLIGGNRLKOPPECMEDVYDL 750
0Y 742 MYOCMSADPKRPSFTCLRMLENIITGLSIVLSASODPLYINIERAEPEPAGSGLELPER 801
Db 751 MYOCMSADPKRPSFTCLRMLENIITGLSIVLSASODPLYINIERAEPEPAGSGLELPER 810
0Y 802 DQPYSGAGDGSGMGAVGTPSDCRYILTPGIALEOPGAEHOPESEPLNTORLLILQGL 861
Db 811 DQPYSGAGDGSGMGAVGTPSDCRYILTPGIALEOPGAEHOPESEPLNTORLLILQGL 870
0Y 862 LPHSSC 867
Db 871 LPHSSC 876

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RESULT 3
 R60548
 ID R60548 standard; Protein; 850 AA.
 AC R60548;
 DT 14-APR-1995 (first entry)
 DE Mature human developmental tyrosine kinase (Dtk).
 KW Receptor tyrosine kinase; developmental tyrosine kinase;
 KM vertebrate development.
 OS Homo sapiens.
 PN M09419463-A.
 PD 01-SEP-1994.
 PF 16-FEB-1994; NZ0009.
 PR 16-FEB-1993; NZ-245917.
 PA (AOCK-) AUCKLAND UNISERVICES LTD.
 PI CROSIER KE, CROSIER PS,
 DR WPI: 94-294328/36.
 PR -PSDB; Q71335.
 PT Developmental tyrosine kinase(s) and their ligands - used to
 PT stimulate the proliferation/differentiation or survival of foetal
 or adult neuronal cells of cells that form part of the CNS
 PS Claim 5; Page 64-67; 86pp; English.
 CC Dtk is a transmembrane receptor tyrosine kinase whose extracellular
 domains contain two immunoglobulin-like motifs followed by two
 fibronectin-type III repeats. It is distinguished from RTKs having
 the equivalently structured extracellular domains by its potential
 CC function based upon its distribution within the mammalian body. (RTK
 CC = receptor tyrosine kinase).
 Sequence 850 AA:

Query Match	51.3%	Score 2399;	DB 1;	Length 850;
Best Local Similarity	95.9%	Pred. No. 7.6e-200;		
Matches 466; Conservative	4;	Mismatches 16;	Indels 0;	Gaps 0

QY	382	FSDNADSFYSVOOQNSNPFRMYVYGVLTATVTAALATLLKRRKKRRFGQAF	441
Db	365	WSQPLVSSSHBRAGQGGQPPSRSTSWPVPVLTGLTALVTAALATLLKRRKKRRFGQAF	424
QY	442	DSVMARGEPAVHFRASFSRRRPERPERATLISGIDSLKFKLEDVILPPOQFTGLRML	501
Db	425	DSVMARGEPAVHFRASFSRRRPERPERATLISGIDSLKFKLEDVILPPOQFTGLRML	484
QY	502	GKGEFGVREANLQEOGGSVYKAVYKMLKADITIASDILEEFLRPAQCKKEFDHRYAKYL	561

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Db 485 GGEESVREAGLQKEDSSFVAVKMKADIIASSDIEEFLEAAKKEFDHPHAKLV 544
QY 563 GVSLSRAKGRLPIMVILPFMKHGDHLAFLASRIGENPNFLPQTLIRFVADIACME 621
Db 545 GVSLSRAKGRLPIMVILPFMKHGDHLAFLASRIGENPNFLPQTLIRFVADIACME 604
QY 632 YLSRNFHRLDLAARNCLAEADMTVCVADFGLSRKISGDIYRGOCASKLIPVKWLALESL 681
Db 605 YLSRNFHRLDLAARNCLAEADMTVCVADFGLSRKISGDIYRGOCASKLIPVKWLALESL 664
QY 662 ADNLYTQSDVMAFGVTMWEITRGQTPYAGIENAEIYNILIGNRKLKOPPECKEEDVYL 741
Db 665 ADNLYTQSDVMAFGVTMWEITRGQTPYAGIENAEIYNILIGNRKLKOPPECKEEDVYL 724
QY 742 MYCKMSADPKORPSTFCLRMELNITLGLSVLSASODPLYNIRAEPTAGSLELPGR 801
Db 725 MYCKMSADPKORPSTFCLRMELNITLGLSVLSASODPLYNIRAEPTAGSLELPGR 784
QY 802 DOPYSGAGDSGGMAGVGTSPDCRYILTPGGLAEQPGQAEHPESPPLNETORLLLOGL 861
Db 785 DOPYSGAGDSGGMAGVGTSPDCRYILTPGGLAEQPGQAEHPESPPLNETORLLLOGL 844
QY 862 LPHSSC 867
Db 845 LPHSSC 850

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RESULT 4

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ID R60545 standard; Protein; 874 AA.
AC R60545;
DE 14-APR-1995 (first entry)
DE Murine developmental tyrosine kinase (Dtk).
KW Receptor tyrosine kinase; developmental tyrosine kinase;
KW vertebrate development.
OS Mus musculus.
PN MO9419463-A.
PD 01-SEP-1994.
PE 16-FEB-1994; NZ-245917.
PR 16-FEB-1993; NZ-245917.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
PI Crosier KE, Crosier PS;
DR WPI: 94-294328/36.
DR N-PSDB: 071332.
PT Developmental tyrosine kinase(s) and their ligands - used to
stimulate the proliferation differentiation or survival of foetal
or adult neuronal cells of cells that form part of the CNS
PS Claim 2; Page 53-57; 86pp; English.
CC Dtk is a transmembrane receptor tyrosine kinase whose extracellular
domains contain two immunoglobulin-like motifs followed by two
fibronectin-type III repeats. It is distinguished from RTKs having
CC the equivalently structured extracellular domains by its potential
CC function based upon its distribution within the mammalian body. (RTK
CC = receptor tyrosine kinase).
SQ Sequence 874 AA;

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Query Match 48.0%; Score 2246; DB 1; Length 874;
Best Local Similarity 90.1%; Pred. No. 1.6e-186;
Matches 438; Conservative 14; Mismatches 34; Indels 0; Gaps 0;
QY 382 FSDQMDSTFSVVOONSNPAMRAWVYVGLVLTALVTAALAILILRKRRKTRFGQAF 441
Db 389 WSOPLVYSSHDHAGRGOPHSRTSWPVVGLVLTALVTAALAILILRKRRKTRFGQAF 448
QY 442 DSVNAGEPAVHRRAASFNRERPERIEATLDSIGISDELKELDEVILPEQOFTLGRML 501
Db 449 DSVNAGEPAVHRRAASFNRERPERIEATLDSIGISDELKELDEVILPEQOFTLGRML 508
QY 502 GKGEFSGVREAOIKOEDGSFVAVKMKADIIASSDIEEFLEAAKKEFDHPHAKLV 561
Db 509 GKGEFSGVREAOIKOEDGSFVAVKMKADIIASSDIEEFLEAAKKEFDHPHAKLV 568

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QY 562 GVSLSRAKGRLPIMVILPFMKHGDHLAFLASRIGENPNFLPQTLIRFVADIACME 621
Db 569 GVSLSRAKGRLPIMVILPFMKHGDHLAFLASRIGENPNFLPQTLIRFVADIACME 628
QY 622 YLSRNFHRLDLAARNCLAEADMTVCVADFGLSRKISGDIYRGOCASKLIPVKWLALESL 681
Db 629 YLSRNFHRLDLAARNCLAEADMTVCVADFGLSRKISGDIYRGOCASKLIPVKWLALESL 688
QY 682 ADNLYTQSDVMAFGVTMWEITRGQTPYAGIENAEIYNILIGNRKLKOPPECKEEDVYL 741
Db 689 ADNLYTQSDVMAFGVTMWEITRGQTPYAGIENAEIYNILIGNRKLKOPPECKEEDVYL 748
QY 742 MYCKMSADPKORPSTFCLRMELNITLGLSVLSASODPLYNIRAEPTAGSLELPGR 801
Db 749 MYCKMSADPKORPSTFCLRMELNITLGLSVLSASODPLYNIRAEPTAGSLELPGR 808
QY 802 DOPYSGAGDSGGMAGVGTSPDCRYILTPGGLAEQPGQAEHPESPPLNETORLLLOGL 861
Db 809 ERSSSEAGDSGGMAGVGTSPDCRYILTPGGLAEQPGQAEHPESPPLNETORLLLOGL 868
QY 862 LPHSSC 867
Db 869 LPHSSC 874

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RESULT 5

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ID R60546 standard; Protein; 850 AA.
AC R60546;
DE 14-APR-1995 (first entry)
DE Mature murine developmental tyrosine kinase (Dtk).
KW Receptor tyrosine kinase; developmental tyrosine kinase;
KW vertebrate development.
OS Mus musculus.
PN MO9419463-A.
PD 01-SEP-1994.
PE 16-FEB-1994; NZ-245917.
PR 16-FEB-1993; NZ-245917.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
PI Crosier KE, Crosier PS;
DR WPI: 94-294328/36.
DR N-PSDB: 071333.
PT Developmental tyrosine kinase(s) and their ligands - used to
stimulate the proliferation differentiation or survival of foetal
or adult neuronal cells of cells that form part of the CNS
PS Claim 3; Page 57-60; 86pp; English.
CC Dtk is a transmembrane receptor tyrosine kinase whose extracellular
domains contain two immunoglobulin-like motifs followed by two
fibronectin-type III repeats. It is distinguished from RTKs having
CC the equivalently structured extracellular domains by its potential
CC function based upon its distribution within the mammalian body. (RTK
CC = receptor tyrosine kinase).
SQ Sequence 850 AA;

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Query Match 48.0%; Score 2246; DB 1; Length 850;
Best Local Similarity 90.1%; Pred. No. 1.5e-186;
Matches 438; Conservative 14; Mismatches 34; Indels 0; Gaps 0;
QY 382 FSDQMDSTFSVVOONSNPAMRAWVYVGLVLTALVTAALAILILRKRRKTRFGQAF 441
Db 365 WSOPLVYSSHDHAGRGOPHSRTSWPVVGLVLTALVTAALAILILRKRRKTRFGQAF 424
QY 442 DSVNAGEPAVHRRAASFNRERPERIEATLDSIGISDELKELDEVILPEQOFTLGRML 501
Db 425 DSVNAGEPAVHRRAASFNRERPERIEATLDSIGISDELKELDEVILPEQOFTLGRML 484
QY 502 GKGEFSGVREAOIKOEDGSFVAVKMKADIIASSDIEEFLEAAKKEFDHPHAKLV 561
Db 485 GKGEFSGVREAOIKOEDGSFVAVKMKADIIASSDIEEFLEAAKKEFDHPHAKLV 544
QY 562 GVSLSRAKGRLPIMVILPFMKHGDHLAFLASRIGENPNFLPQTLIRFVADIACME 621

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Db 545 GVSLSRAKGRLPIMVILPFMKGDLHAFLASRIGENFNLQTLVRFWDIACGM 604
QY 622 YLSRNFIRHDLAARNCLAEEDMTVCVADFGLSRKRIYSGDYRGCASKLPEVKLAE 681
Db 605 YLSRNFIRHDLAARNCLAEEDMTVCVADFGLSRKRIYSGDYRGCASKLPEVKLAE 664
QY 682 ADNLTYVSDVMAFGVTMELMTRGOTPYAGIENAEIYNYLIGNRKLPKPECEMDY 741
Db 665 ADNLTYVSDVMAFGVTMELMTRGOTPYAGIENAEIYNYLIGNRKLPKPECEMDY 724
QY 742 MYQCSADPKRPSFTCLRMELNITLIGLSVLSASQDPLYNITERAEPTAGSLE 801
Db 725 MYQCSADPKRPSFTCLRMELNITLIGLSVLSASQDPLYNITERAEPTAGSLE 784
QY 802 DQPYGAGDGSQMGAVGTPSDCRITLTPGGLAEQPGQAEHOPESPPLNETORLL 861
Db 785 ERSSEADGDSQMGAVGTPSDCRITLTPGGLAEQPGQAEHOPESPPLNETORLL 844
QY 862 LPHSSC 867
845 LPHSSC 850

RESULT 6
R77846
ID R77846 standard; Protein; 880 AA.
AC R77846;
DE 01-NOV-1995 (first entry)
DE Mouse Rse rPRK.
KM RSE: receptor protein tyrosine kinase; rPRK; diagnostic; therapy;
KM neurodegenerative disease; Alzheimer disease; Parkinson disease;
KM kidney disease.
OS Mus sp.
FH Key
FH peptide
FT modified_site 1..30 Location/Qualifiers
FT modified_site 53 /label- Sig_peptide
FT modified_site 73 /label- N-glycosylation_site
FT modified_site 181 /label- N-glycosylation_site
FT modified_site 220 /label- N-glycosylation_site
FT modified_site 230 /label- N-glycosylation_site
FT modified_site 283 /label- N-glycosylation_site
FT modified_site 356 /label- N-glycosylation_site
FT modified_site 370 /label- N-glycosylation_site
FT modified_site 419..441 /label- N-glycosylation_site
FT domain 508..775 /label- Transmembrane_domain
FT domain 515..520 /label- Tyrosine_kinase_domain
FT binding_site /label- Mg2+-ATP_binding_site
FT
FT WO9514776-A.
PN 01-JUN-1995.
PD 15-NOV-1994; U13214.
PR 23-NOV-1993; US-157563.
PR 20-DEC-1993; US-170558.
PR 05-AUG-1994; US-286305.
PR (GETH ) GENENTECH INC.
PA (NEMO-) NEW ENGLAND DEACONESS HOSPITAL.
PI Godowski PJ, Mark MR, Scadden DT, Sackik MD, Wong WLT;
DR WPI: 95-206933/27.
DR N-PSDB; Q94422.
PT Human and murine receptor protein tyrosine kinase(s) and corresp. DNA -
PT for stimulation of cell growth and differentiation e.g. for treatment of
PT neurodegenerative and kidney diseases

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PS Claim 6; Fig.1B; 119pp; English.
CC The murine homolog (given in Q94422) of human Rse cDNA (Q94421) was
CC obtd. from a brain cDNA library using the human Rse cDNA as probe.
SQ Sequence 880 AA;

Query Match          47.9%; Score 2239; DB 1; Length 880;
Best local similarity 89.9%; Pred No.6.5e-166;
Matches 437; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 382 FSDMADSFSTFYVQONSPPANRAMPVVLGVLTALVTAAALILIRKRETRFGQAF 441
Db 395 WSGPLVYSSHDHNRGQPHRSRTSWPVVLGVLTALVTAAALILIRKRETRFGQAF 454
QY 442 DSYMARGEPAVHFRAARSRRRPERIENTLDSLGISDELKEDVLIPEQOFTLGRML 501
Db 455 DSYMARGEPAVHFRAARSRRRPERIENTLDSLGISDELKEDVLIPEQOFTLGRML 514
QY 502 GKGEFVSREAOLOKEDGSFVAVKMLKADIIASSDIIEEFREAACKEDPHVATLY 561
Db 515 GKGEFVSREAOLOKEDGSFVAVKMLKADIIASSDIIEEFREAACKEDPHVATLY 574
QY 562 GVSLSRAKGRLPIMVILPFMKGDLHAFLASRIGENFNLQTLVRFWDIACGM 621
Db 575 GVSLSRAKGRLPIMVILPFMKGDLHAFLASRIGENFNLQTLVRFWDIACGM 634
QY 622 YLSRNFIRHDLAARNCLAEEDMTVCVADFGLSRKRIYSGDYRGCASKLPEVKLAE 681
Db 635 YLSRNFIRHDLAARNCLAEEDMTVCVADFGLSRKRIYSGDYRGCASKLPEVKLAE 694
QY 682 ADNLTYVSDVMAFGVTMELMTRGOTPYAGIENAEIYNYLIGNRKLPKPECEMDY 741
Db 695 ADNLTYVSDVMAFGVTMELMTRGOTPYAGIENAEIYNYLIGNRKLPKPECEMDY 754
QY 742 MYQCSADPKRPSFTCLRMELNITLIGLSVLSASQDPLYNITERAEPTAGSLE 801
Db 755 MYQCSADPKRPSFTCLRMELNITLIGLSVLSASQDPLYNITERAEPTAGSLE 814
QY 802 DQPYGAGDGSQMGAVGTPSDCRITLTPGGLAEQPGQAEHOPESPPLNETORLL 861
Db 815 ERSSEADGDSQMGAVGTPSDCRITLTPGGLAEQPGQAEHOPESPPLNETORLL 874
QY 862 LPHSSC 867
875 LPHSSC 880

RESULT 7
W79145
ID W79145 standard; Protein; 874 AA.
AC W79145;
DE 19-NOV-1998 (first entry)
DE Receptor protein tyrosine kinase (PTK) subtype tyro-3.
KM PTK; receptor; protein tyrosine kinase; brain tissue.
OS Rattus sp.
PN US581516-A.
PD 22-SEP-1998.
PR 02-JUN-1995; 456647.
PR 15-MAY-1992; US-884486.
PR 02-MAY-1994; US-237401.
PR 02-JUN-1995; US-456647.
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
PI Lai CHC, Lemke GE;
DR WPI: 98-530939/45.
DR N-PSDB; V53888.
PT Receptor protein tyrosine kinase polypeptide, tyro-3 - preferably
PT expressed in brain tissue
PS Claim 3; Columns 33-40; 46pp; English.
CC This represents a novel receptor protein tyrosine kinase (PTK)
CC polypeptide subtype tyro-3. The invention provides polynucleotide
CC sequences encoding novel PTK polypeptide subtypes tyro-1 to tyro-13.
CC The PTK subtypes are found expressed predominantly in the brain tissue.
SQ Sequence 874 AA;

```

Query Match 47.9%; Score 2238; DB 1; Length 874;
 Best Local Similarity 89.7%; Pred. No. 7.9e-186;
 Matches 436; Conservative 15; Mismatches 35; Indels 0; Gaps 0;

CC the protein expressed, and expression products screened for using
 CC antibodies against tyrosine kinase epitopes. These subtypes sequences can
 CC be used for the design of oligonucleotides, for use in amplification
 CC reactions to isolate other subtype sequences. These detection protocols
 CC are used in the diagnosis of diseases associated with (receptor) PKs.
 CC Recombinant vectors expressing the subtypes can be used to treat related
 CC diseases e.g. tumours, by introduction of the vectors into skin
 CC transplants, then grafting these into the connective tissue of the
 CC dermis, thus specifically targeting tumours as the proteins are released
 CC from the matrix.

CC Sequence 874 AA:

DB 382 FSQDMADSTFVVOQONSFPAMRAVAVVGVLTALTAALAILLKRKRKTRFGQAF 441
 DB 389 WSQPLVYSSHDHAGRQPPHSRTSWVPVVLGYLTALTAALAILLKRKRKTRFGQAF 448
 QY 442 DSVNARGEPAVHFRARSFNRRPERIEATLDSLGISDELKEDVLIPEQFTLGRML 501
 DB 449 DSVNARGEPAVHFRARSFNRRPERIEATLDSLGISDELKEDVLIPEQFTLGRML 508
 QY 502 GKGEFGSVREAOIKOEDGSFVKAVKMLKADIIASSDIEEFLEAKCKEFDHPHAKVY 561
 DB 509 GKGEFGSVREAOIKOEDGSFVKAVKMLKADIIASSDIEEFLEAKCKEFDHPHAKVY 568
 QY 562 GVSLSRAKGRPLIPVILPFMKHGDHLAFLASRIGENFNPLOTILRFMDIAGME 621
 DB 569 GVSLSRAKGRPLIPVILPFMKHGDHLAFLASRIGENFNPLOTILRFMDIAGME 628
 QY 622 YLSSRNFIRHDLAARNCMLAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 681
 DB 629 YLSSRNFIRHDLAARNCMLAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 688
 QY 682 ADNLITYVQSDVNAFVGTWMEINTRGOTPYAGIENAEIYNYLIGNRKLOPECEMEDYDL 741
 DB 689 ADNLITYVQSDVNAFVGTWMEINTRGOTPYAGIENAEIYNYLIGNRKLOPECEMEDYDL 748
 QY 742 MYQCMSADPKRPSFTCLMELENIIGOLSVLASODPLYINIRAEPTAGSLELPGR 801
 DB 749 MYQCMSADPKRPSFTCLMELENIIGOLSVLASODPLYINIRAEPTAGSLELPGR 808
 QY 802 DQPYSGADGSGMGAVGTPSDCRITLTPGGLAEOPOGAEOHPESPENORLLLLQOGL 861
 DB 809 ERSSSEAGDGSVGAVGIPSDSRITYSPGLSESPGLEQEPSPLENORLLLLQOGL 868
 QY 862 LPHSSC 867
 DB 869 LPHSSC 874

RESULT 8
 ID W81402
 W81402 standard; Protein: 874 AA.

CC Receptor protein tyrosine kinase (PTK) subtype tyro-3.
 CC PK; receptor; protein tyrosine kinase; recombinant; grafting;
 CC diagnosis; tumour; skin transplant; connective tissue; tyro-3.
 CC Rattus sp.
 CC US5837448-A.
 CC 17-NOV-1998.
 CC 02-MAY-1994; 237401.
 CC 15-MAY-1992; US-884486.
 CC 02-MAY-1994; US-237401.
 CC (SALK) SALK INST BIOLOGICAL STUDIES.
 CC LAI CHC, Lemke GE;
 CC WPI: 99-023436/02.
 CC N-PSDB; V65310.
 CC Nucleic acids encoding protein tyrosine kinase subtypes - for
 CC identification of new subtypes and treatment of diseases associated
 CC with the kinase
 CC Claim 10; Columns 33-40; 47pp; English.
 CC This represents a receptor protein tyrosine kinase (PTK) subtype tyro-3.
 CC The invention provides sequences V65308 to V65313, V65315, and V65317 to
 CC V65319 that encode proteins having a tyrosine kinase domain and a tissue
 CC expression pattern of a receptor PTK subtype selected from tyro-1, and
 CC tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10, tyro-11, and
 CC tyro-12, respectively. The polynucleotides are useful for the detection
 CC of tyrosine kinase domain sequences and detection of tissue expression
 CC patterns of PTK subtypes. The cDNAs can also be injected into oocytes,

CC the protein expressed, and expression products screened for using
 CC antibodies against tyrosine kinase epitopes. These subtypes sequences can
 CC be used for the design of oligonucleotides, for use in amplification
 CC reactions to isolate other subtype sequences. These detection protocols
 CC are used in the diagnosis of diseases associated with (receptor) PKs.
 CC Recombinant vectors expressing the subtypes can be used to treat related
 CC diseases e.g. tumours, by introduction of the vectors into skin
 CC transplants, then grafting these into the connective tissue of the
 CC dermis, thus specifically targeting tumours as the proteins are released
 CC from the matrix.

CC Sequence 874 AA:

DB 382 FSQDMADSTFVVOQONSFPAMRAVAVVGVLTALTAALAILLKRKRKTRFGQAF 441
 DB 389 WSQPLVYSSHDHAGRQPPHSRTSWVPVVLGYLTALTAALAILLKRKRKTRFGQAF 448
 QY 442 DSVNARGEPAVHFRARSFNRRPERIEATLDSLGISDELKEDVLIPEQFTLGRML 501
 DB 449 DSVNARGEPAVHFRARSFNRRPERIEATLDSLGISDELKEDVLIPEQFTLGRML 508
 QY 502 GKGEFGSVREAOIKOEDGSFVKAVKMLKADIIASSDIEEFLEAKCKEFDHPHAKVY 561
 DB 509 GKGEFGSVREAOIKOEDGSFVKAVKMLKADIIASSDIEEFLEAKCKEFDHPHAKVY 568
 QY 562 GVSLSRAKGRPLIPVILPFMKHGDHLAFLASRIGENFNPLOTILRFMDIAGME 621
 DB 569 GVSLSRAKGRPLIPVILPFMKHGDHLAFLASRIGENFNPLOTILRFMDIAGME 628
 QY 622 YLSSRNFIRHDLAARNCMLAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 681
 DB 629 YLSSRNFIRHDLAARNCMLAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 688
 QY 682 ADNLITYVQSDVNAFVGTWMEINTRGOTPYAGIENAEIYNYLIGNRKLOPECEMEDYDL 741
 DB 689 ADNLITYVQSDVNAFVGTWMEINTRGOTPYAGIENAEIYNYLIGNRKLOPECEMEDYDL 748
 QY 742 MYQCMSADPKRPSFTCLMELENIIGOLSVLASODPLYINIRAEPTAGSLELPGR 801
 DB 749 MYQCMSADPKRPSFTCLMELENIIGOLSVLASODPLYINIRAEPTAGSLELPGR 808
 QY 802 DQPYSGADGSGMGAVGTPSDCRITLTPGGLAEOPOGAEOHPESPENORLLLLQOGL 861
 DB 809 ERSSSEAGDGSVGAVGIPSDSRITYSPGLSESPGLEQEPSPLENORLLLLQOGL 868
 QY 862 LPHSSC 867
 DB 869 LPHSSC 874

RESULT 9
 ID Y07286
 Y07286 standard; Protein: 887 AA.

CC Human brain-specific tyrosine kinase (BTK) protein.
 CC Human; brain; tyrosine kinase; BTK; drug application; antigen;
 CC Human samples.
 CC J08356780-A.
 CC 08-OCT-1996.
 CC 17-MAR-1995; 097411.
 CC 17-MAR-1995; JP-097411.
 CC (CHUS) CHUGAI PHARM CO LTD.
 CC WPI: 96-500368/50.
 CC N-PSDB; X07286.
 CC Gene coding brain-specific tyrosine kinase - can be used to detect
 CC nervous skin syndrome related antigen
 CC Disclosure; Fig 8; 31pp; Japanese.

nerve cells

KW neuromuscular disorder; diabetes; glaucoma; sensory neuron;
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
KW neurotrophin; signal transduction; dopaminergic nerve cell;

KM neurological disorder; diabetes; glaucoma; sensory neuron;
KM retinal ganglion cell degeneration; sensory neuropathy;
KM retinopathy; gene therapy; GDNF-related protein 3; GRR3.

OS Rattus sp.
 PN W09854213-A2.
 PD 03-DEC-1998.
 PF 27-APR-1998; U08486.
 PR 30-MAY-1997; US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR WPI; 99-080806/07.
 DR N-PSDB: V99331.
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 PT used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 PS or amyotrophic lateral sclerosis.
 PS Claim 51; Fig 17; 31pp; English.
 CC The present sequence represents a rat glial cell-line derived
 CC neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3).
 CC The protein has similar functions to GDNFR. GDNFR proteins are
 CC functionally characterised by the ability to bind glial cell
 CC line-derived neurotrophic factor (GDNF) and/or neuritin specifically,
 CC and to act as part of a molecular complex which mediates or enhances
 CC the signal transduction affects of GDNF and/or neuritin. The proteins
 CC can be used for treating improperly functioning dopaminergic nerve
 CC cells, Parkinson's disease, Alzheimer's disease or amyotrophic lateral
 CC sclerosis. They can also be used for treating neurological disorders
 CC associated with diabetes, glaucoma or other diseases and conditions
 CC involving retinal ganglion cell degeneration, sensory neuropathy caused
 CC by injury to, insults to, or degeneration of, sensory neurons.
 CC pathological conditions, or disease or injury-related retinopathies.
 CC The products can also be used for detection, diagnosis, drug screening
 CC and gene therapy.
 SQ Sequence 397 AA;

Query Match 38.1%; Score 1779; DB 1; Length 397;
 Best Local Similarity 89.4%; Pred. No. 1,8e-146;
 Matches 336; Conservative 11; Mismatches 23; Indels 6; Gaps 2;

OY 54 LEAGNSLATEENRFVNSTQARKKCEANPACKAAYQHLSCTSSLSRPLPESAMSADCL 113
 DB 25 LGTGNLSPEENRLVNSTQARKKCEANPACKAAYQHLSCTSSLSRPLPESAMSADCL 84
 OY 114 EAAEOLNSSLIDCRCHRRKHQATCLDIYVTHPARSLDYELDYSPEYDVTSPKMK 173
 DB 85 EAAQOLNSSLIDCRCHRRKHQATCLDIYVTHPARSLDYELDYSPEYDVTSPKMK 144
 OY 174 NLSKIMLKRSDSLCKFALMCTLHDKCDLRAAYGACGICORHLCLAQSRFFEXA 233
 DB 145 NLSKIMLKRSDSLCKFALMCTLHDKCDLRAAYGACGICORHLCLAQSRFFEXA 204
 OY 234 AESHAOGLLCPPEPDAGCGERRRNTIAPSCALPSTPCLDLRSGCRADPLCRSLMD 293
 DB 205 AESHAOGLLCPPEPDAGCGERRRNTIAPSCALPSTPCLDLRSGCRADPLCRSLMD 264
 OY 294 FQTHCHPMDLIGTCATEQSRCLRAVILGISTAMTPEFISKVNTTVALSTCRSGSLNLODE 353
 DB 265 FQTHCHPMDLIGTCATEQSRCLRAVILGISTAMTPEFISKVNTTVALSTCRSGSLNLODE 324
 OY 354 CELELESFSGNPLVLAIAAKAFHROLSQMDADSTFVSVOQNSNPAMRAVPPVVLGV 413
 DB 325 CELELESFSGNPLVLAIAAKAFHROLSQMDADSTFVSVOQNSNPALRP--QLRLPV 382
 OY 414 LVALVTAALALILRL 429
 DB 383 LSEFFI-----LTLLILO 394

RESULT 12
 ID W37465
 AC W37465 standard; Protein: 346 AA.
 DT 21-MAY-1998 (first entry)
 DE Mouse Ret ligand ret3 partial sequence.
 KW Ret ligand; Ret3; receptor; signal transduction; mouse;

KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Mus musculus.
 PN W09744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIO) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nadel M;
 DR WPI; 98-018431/02.
 DR N-PSDB: V00256.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Disclosure; Page 73-74; 113pp; English.
 CC This polypeptide comprises a partial sequence of mouse Ret ligand
 CC Ret3, deduced from EST AA050083 cDNA (see V00256). A full-length
 CC mouse Ret3 sequence (see W37461) was also obtained. Rat, mouse
 CC and human Ret1, Ret2 and Ret3 cDNA sequences (see V00245-51) and
 CC encoded polypeptides (see W37457-63) are claimed and can be used
 CC in methods for promoting cell growth and improving survival of
 CC cells, especially renal or neural cells.
 SQ Sequence 346 AA;

Query Match 35.5%; Score 1658; DB 1; Length 346;
 Best Local Similarity 93.7%; Pred. No. 4,9e-136;
 Matches 312; Conservative 5; Mismatches 10; Indels 6; Gaps 1;

OY 97 LSRPLPESAMSADCLAEAEOLNSSLIDCRCHRRKHQATCLDIYVTHPARSLDY 156
 DB 17 LSRPLPESAMSADCLAEAEOLNSSLIDCRCHRRKHQATCLDIYVTHPARSLDY 76
 OY 157 LDVSPEDYVTSKPMWNLSTKLMLKPSDCLCKFALMCTLHDKCDLRAAYGACSGIR 216
 DB 77 LDVSPEDYVTSKPMWNLSTKLMLKPSDCLCKFALMCTLHDKCDLRAAYGACSGIR 136
 OY 217 CORHLCLAQSRFFEXAASHAQGLLCPPEPDAGCGERRRNTIAPSCALPSTPNCID 276
 DB 137 CORHLCLAQSRFFEXAASHAQGLLCPPEPDAGCGERRRNTIAPSCALPSTPNCID 196
 OY 277 LNSFCRADPLCRSLMDFTCHPMDLIGTCATEQSRCLRAVILGISTAMTPEFISKVNT 336
 DB 197 LNSFCRADPLCRSLMDFTCHPMDLIGTCATEQSRCLRAVILGISTAMTPEFISKVNT 256
 OY 337 TYALSTCGSGNLQDECOLERSQNCVLEAIAAKAFHROLSQMDADSTFVSVOQ 396
 DB 257 TYALSTCGSGNLQDECOLERSQNCVLEAIAAKAFHROLSQMDADSTFVSVOQ 316
 OY 397 QNSNPAMRAVPPVVLGVLTALVTAALALILRL 429
 DB 317 QNSNPALR-----LQRLPIILSFTLLPILLO 343

RESULT 13
 ID W37463
 AC W37463 standard; Protein: 400 AA.
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand Ret3.
 KW Ret ligand; Ret3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;

EW	Infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;	
EW	cranial nerve injury; spinal cord injury; Down's syndrome;	
EW	cerebral palsy; Lyme disease; muscular dystrophy;	
OS	myasthenia gravis; tumour; therapy.	
KN	Homo sapiens.	
PN	W09744356-A2.	
PD	27-NOV-1997.	
PF	07-MAY-1997; U07726.	
PR	10-MAR-1997; US-017427.	
PR	08-MAY-1996; US-017427.	
ER	07-JUN-1996; US-019300.	
ER	16-JUL-1996; US-021859.	
PA	(BIOJ) BIOGEN INC.	
PR	Cate RL, Hession C, Santicola-Nadel M;	
DR	WPI: 98-018431/02.	
DR	N-PDB: V00251.	
PT	New nucleic acid encoding ret receptor ligands and related proteins	
PT	-vectors, transformed cells and antibodies, used for promoting cell	
PT	growth and improving survival of injured cells, especially renal or	
PT	nerve cells	
	Claim 2: Page 85-86; 113pp: English.	
CC	This amino acid sequence comprises human Ret ligand (Ret), Ret3,	
CC	deduced from cDNA clones (see V00251) isolated from a adult heart	
CC	and spinal cord libraries. Rat and human Ret1, human Ret2 and	
CC	mouse Ret3 sequences (see W37457-62) are also claimed. Human	
CC	Ret3 is 34.3% identical to human Ret1, 34.9% identical to human	
CC	Ret2 and 76.8% identical to murine Ret3. Ret ligand is a key	
CC	component of the Ret signalling pathway that specifically	
CC	interacts with Ret receptor protein, triggering Ret dimerisation	
CC	and/or autophosphorylation of the Ret tyrosine kinase domain.	
CC	Vectors containing ret3 DNA and prokaryotic or eukaryotic host	
CC	cells transformed or transfected with these vectors are claimed, as	
CC	well as a method for production of Ret3, its soluble variants and	
CC	fusion proteins with a toxin, imageable compound or radionuclide.	
CC	Ret3, optionally when expressed from vectors in vivo, is used to	
CC	promote growth of new tissue and survival of damaged tissue.	
CC	Particularly, kidney or neural tissue. Typical applications are in	
CC	renal failure, nephritis, kidney transplants, toxic or hypoxic	
CC	injury, neurodegeneration, motor neurone disease, multiple sclerosis	
CC	bacterial, viral or prion infections (e.g. meningitis, myelopathy	
CC	associated with HIV or Creutzfeldt-Jakob disease), myelopathy	
CC	spinal cord injury, developmental disorders such as Down's syndrome	
CC	and cerebral palsy, or conditions involving the peripheral nervous	
CC	system (Lyme disease, muscular dystrophy and myasthenia gravis).	
CC	Fusion proteins are used to deliver toxins etc. to Ret-expressing	
CC	cells, especially tumours.	
SC	Sequence 400 AA;	

QY	very Match	33.5%;	Score 1567;	DB 1;	Length 400;
QY	est Local Similarity	76.08;	Pred. No. 5e-128;		
QY	Matches 292;	Conservative 26;	Mismatches 56;	Indels 10;	Gaps
QY	47 LPVLDLLEAGNSLATEENREYVNSTQVARKKCEANPACKAAVYHILGTSSTLSRLPLEES	1068			
DB	21 LPSPPLPLAADPPTESRLNNSGLOARRKQADPTCSAAVHHDSCTSSISTPLPEEP	80			
QY	107 AMSADCEAAQOLNNSISIDRCRRKKHQATCIDYWTYHPRASLDYELDYSPYEDYV	1668			
DB	81 SVRSDCEAAQOLNNSISIDRCRRKKNOVACDIYWTYHPRASLDYELDYSPYEDYV	1404			
QY	167 TSKRWKNNLSKLNALKEPDSIDCLTFAMVLCITLHDKCDLRLRAYGAGCGISGQRHLCALQ	2268			
DB	141 TSKRWKNNLSKLNALKEPDSIDCLTFAMVLCITLHDKCDLRLRAYGAGCGISGQRHLCALQ	2000			
QY	227 RSFEKKAESAAGCLLCPCEPPEAGCGERRRNTIAPSCALPSYTPNCIDLRSCFADPL	2866			
DB	201 LTFEKAEPAPAGCLLCPAPANDRGGERRRNTIAPNCALPVPAPNCLTRLRCSFDPL	2606			
QY	287 CSRRLDQFOTRHCHPMDLIGTCATQSSCLRAYGLISTANTPNPISVNTVALLSCGCG	3466			
DB	261 CSRRLDQFOTRHCHPMDLIGTCATQSSCLRAYGLISTANTPNPISVNTVALLSCGCG	3200			

QY	347	SGNLODEECOLESEFSONPCTVATAIAKAKRERHOLFSDQMDADSTFSVQOONSIPAKR--	405
Db	321	SGNLODEECOLESEFSONPCTVATAIAKAKRERHOLFSDQMDADSTFSVQOONSIPAKR	380
QY	405	AMVPVYLGVLTAALTAALALAILL 428	
Db	381	FMVPSLF-----SCTLELILL 396	
RESULT	14		
ID	W5116	W5116 standard; Protein; 400 AA.	
AC	W5116		
DT	28-SEP-1998	(first entry)	
DE	Human GDNF alpha-3 receptor protein #1.		
KW	Gliatal cell line-derived neurotrophic factor alpha-3 receptor; GDNF;		
KW	treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;		
KW	amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;		
KW	Huntington's disease; Alzheimer's disease; diabetic neuropathy; muscle		
OS	muscular dystrophy; diagnostic.		
FX	Homo sapiens.		
FX	Key	Location/Qualifiers	
FT	Protein	1..400	
FT		/label= GDNF alpha-3	
FT		/note= "partial sequence"	
PN	EP-846764-A2.		
PD	10-JUN-1998.		
PR	20-NOV-1997.	309375.	
PR	09-MAY-1997.	GB-009463.	
PR	27-NOV-1996.	GB-024677.	
PA	(SMIK) SMITHKLINE BEECHAM PLC.		
PI	Lawrence GMP.		
DR	WPI; 98-299980/27.		
DR	N-PSDB; V35364.		
PT	New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -		
PT	need to treat neuro degenerative diseases, muscular diseases and		
PT	nerve and muscle trauma and in diagnostic assays		
PS	Claim 4; Fig 2; 22pp. English.		
CC	This sequence represents a novel glial cell line-derived neurotrophic		
CC	factor alpha-3 receptor (GDNF alpha-3). This protein can be used to		
CC	treat e.g. neurodegenerative diseases (such as Parkinson's disease,		
CC	amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA),		
CC	Huntington's disease, Alzheimer's disease, diabetic neuropathy), and		
CC	muscular diseases (including the muscular dystrophies) and nerve and		
CC	muscle trauma and in diagnostic assays for such conditions.		
CC	Sequence 400 AA.		

[illegible]

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DB 321 SGNLODECEMLGEGFFSHNCLTEALAKRHFHSQLEFSQMPHPTFAVAHONENPAVRPQ 380
QY 405 AMVPVVLGVLTAALALIL 428
DB 381 PMVPSLF-----SCTLPIL 396

RESULT 15
W84186
W84186 standard; Protein; 400 AA.
AC W84186;
DE 25-MAR-1999 (first entry)
KW Glial cell line-derived neurotrophic factor receptor gamma 2.
KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma2;
KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
KW renal disorder; kidney failure; gut dysfunction; regeneration;
KW cardiomyocyte; epithelium; hepatocyte.
OS Homo sapiens.
FH Key
FT Peptide
FT 1. 31
FT /label- signal_peptide
FT 32. 400
FT /label- mature_protein
FT 32. 382
FT /note- "extracellular domain"
FT 383. 400
FT /note- "transmembrane domain"
PN W09853069-A2.
PD 26-NOV-1998.
PE 20-MAY-1998; U10328.
PR 27-JUN-1997; US-884638.
PR 20-MAY-1997; US-047092.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Gentz RL, Hsu T, Ni J, Ruden SM, Young P;
DR WPI: 99-070150/06.
DR N-PSDB; V99334.
PT New isolated glial cell derived neurotrophic factor receptors - used
PT to develop products for treating e.g. neurodegenerative disorders,
PT schizophrenia, hypertension, tumours, renal disorders, kidney
PT failure or gut dysfunction
PS Clalm 53; F1g 7A-D; 156pp; English.
CC The present sequence represents a glial cell line-derived neurotrophic
CC factor receptor gamma 2 (GDNFR-gamma2). GDNFR-gamma2 shares high homology
CC with GDNFR-alpha, which is capable of complexing with glial cell
CC line-derived neurotrophic factor (GDNF) and mediating cell response to
CC GDNF. The GDNFR polypeptides and agonists can be used for treating
CC disorders associated with decreased activity of the respective
CC polypeptides. They can be used for treating neurodegenerative diseases
CC such as amyotrophic lateral sclerosis, Parkinson's disease,
CC schizophrenia, insomnia, tardive dyskinesia, hypertension, pituitary
CC adenomas, hyperprolactinemia, thyroid tumour, renal disorders, kidney
CC failure, gut dysfunction, or for regeneration of cardiomyocytes,
CC epithelium or hepatocytes. Antagonists of the polypeptides can be used
CC for treating disorders associated with increased activity of the
CC respective polypeptides. The products can also be used for detection,
CC diagnosis and drug screening.
SQ Sequence 400 AA;

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Query Match 33.5%; Score 1567; DB 1; Length 400;
 Best Local Similarity 76.0%; Pred. No. 5e-128;
 Matches 292; Conservative 26; Mismatches 56; Indels 10; Gaps 2;

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QY 47 LPVLDLLEAGNSLATENRFVNSCTOARKKCEANPACKAAYOHLSGCTSSISRLPLEES 106
DB 21 LPPEPLPLAGDPLPTESRLNLSCLQARRKQADPTCSAAYHMLDSCSTISSTPLPSEEP 80
QY 107 AMSADCLAEALQNLNSLIQCRHRKRAKQATCLDIYTWHPARSLGDIYLDVSPYEDTV 166

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DB 81 SVPADCLAEALQNLNSLIQCMCHRMRKNVACLDIYTWHRARSLGVEYLDVSPYEDTV 140
QY 167 TSKPWKMLSKLNMKLPDSDCLKFAMLCTLHDKCDRLRKAYGEGASGIRGCRHCLAQOL 226
DB 141 TSKPWKMLSKLNMKLPDSDCLKFAMLCTLNDKCDRLRKAYGEGASGIRGCRHCLAQOL 200
QY 227 RSFEKKAESHAQGLLCPPEPDAGCGERRRNTIAPSCALPSVTNCLDLRSFCRADPL 286
DB 201 LTFEKAEPHAQGLLCPCAPNDRGCGERRRNTIAPSCALPSVTNCLDLRSFCRADPL 260
QY 287 CRSRLMDPOTCHPMDILGTGATGOSRCLRAYLGLGTAMPTNLSKYNTVAALSCTCRG 346
DB 261 CRSRLVDPOTCHPMDILGTGATGOSRCLRAYLGLGTAMPTNLSKYNTVAALSCTCRG 320
QY 347 SGNLODECEMLGEGFFSHNCLTEALAKRHFHSQLEFSQMPHPTFAVAHONENPAVRPQ 405
DB 321 SGNLODECEMLGEGFFSHNCLTEALAKRHFHSQLEFSQMPHPTFAVAHONENPAVRPQ 380
QY 405 AMVPVVLGVLTAALALIL 428
DB 381 PMVPSLF-----SCTLPIL 396

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 Job time: 446 sec

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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:45:10 ; Search time 20.22 seconds
(without alignments)
1277.366 Million cell updates/sec

Title: US-09-272-835-20

Perfect score: 4675

Sequence: 1 MGSTAAKAGAVILFVYVGL.....DASIKADPNRFGKDLFVL 888

Scoring table: BLOSUM62

Searched: 80000 seqs, 29085965 residues

Database: SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2403	51.4	890	1 TYO3_HUMAN	Q06418 homo sapien
2	2257	48.3	880	1 TYO3_RAT	P55146 rattus norv
3	2246	48.0	880	1 TYO3_MOUSE	P55144 mus musculu
4	1200.5	25.7	887	1 UFO_HUMAN	P30520 homo sapien
5	1178.5	25.2	888	1 UFO_MOUSE	Q00993 mus musculu
6	1061.5	22.7	442	1 RIK_AVIR3	P33497 avian retro
7	646	13.8	370	1 SEA_AVIR2	P23049 avian eryth
8	615.5	13.2	1379	1 MET_MOUSE	P16056 mus musculu
9	612.5	13.1	1367	1 IGIR_HUMAN	P08069 homo sapien
10	610	13.0	2554	1 7LES_DROME	P13368 drosophila
11	609.5	13.0	640	1 IGIR_BOVIN	Q05688 bos taurus
12	606	13.0	1390	1 MET_HUMAN	P08581 homo sapien
13	600	12.8	1400	1 RON_HUMAN	Q04912 homo sapien
14	597.5	12.6	1370	1 IGIR_RAT	P24062 rattus norv
15	590.5	12.6	1115	1 RET_MOUSE	P35546 mus musculu
16	587	12.6	2594	1 7LES_DROI	P08066 drosophila
17	586.5	12.5	1530	1 ABL_DROME	P00522 drosophila
18	583.5	12.5	1382	1 INSR_HUMAN	P06213 homo sapien
19	582	12.4	1372	1 INSR_MOUSE	P15208 mus musculu
20	579.5	12.4	463	1 NTRR_HUMAN	Q00451 homo sapien
21	576.5	12.3	1383	1 NTRR_MOUSE	Q00842 mus musculu
22	575.5	12.3	465	1 NTRR_RAT	P15127 rattus norv
23	575	12.3	507	1 KROS_CHICK	Q13157 gallus gall
24	574.5	12.3	1114	1 RET_HUMAN	P08941 gallus gall
25	573.5	12.3	1300	1 IRR_CAVPO	P07949 homo sapien
26	570.5	12.2	746	1 ABL_MTVAB	P14617 abela porce
27	569	12.2	1123	1 ABL_MOUSE	P00521 mus musculu
28	568.5	12.2	402	1 KROS_AVSU	P00520 mus musculu
29	568.5	12.1	1130	1 ABL_HUMAN	P00529 avian sarco
30	566	12.0	2347	1 KROS_HUMAN	P00519 homo sapien
31	559.5	12.0	1268	1 IRR_HUMAN	P08922 homo sapien
32	550.5	11.8	1363	1 ILPR_RALA	P14616 homo sapien
33	547.5	11.7	1053	1 FAKI_RAT	Q02466 branchiosto
34	547.5	11.7	1124	1 TIR2_HUMAN	Q02763 rattus norv
35	544.5	11.6	1052	1 FAKI_HUMAN	Q00537 mus sapien
36	544.5	11.6	1052	1 FAKI_MOUSE	P34132 mus musculu
37	543.5	11.6	1053	1 FAKI_BOVIN	Q06807 bos taurus
38	540.5	11.6	1053	1 FAKI_CHICK	Q00944 gallus gall
39	539	11.5	1122	1 GDNR_CHICK	Q13156 gallus gall
40	536	11.5	1052	1 TIR2_MOUSE	Q02888 mus musculu
41	535	11.4	819	1 FAKI_XENLA	Q01788 xenopus lae
42	535	11.4	819	1 FGR1_CHICK	P21804 gallus gall

ALIGNMENTS

RESULT	1	STANDARD	PRT	890 AA.
TYO3_HUMAN				
AC	006418			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK).			
GN	TYRO3 OR RSE OR SKY OR DTK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;			
CC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 94193774.			
RA	MARK M.R., SCADEN D.T., WANG Z., GU O., GODDARD A., GODDARD P.J.,			
RT	"RSE, a novel receptor-type tyrosine kinase with homology to Axl/Uto,			
RL	is expressed at high levels in the brain."			
RN	J. Biol. Chem. 269:10720-10728(1994).			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 94150991.			
RA	OHASHI K., MIZUNO K., KUMA K., MIYATA T., NAKAMURA T.;			
RT	"Cloning of the cDNA for a novel receptor tyrosine kinase, sky,			
RL	predominantly expressed in brain."			
RN	Oncogene 9:659-705(1994).			
RP	SEQUENCE FROM N.A.			
RX	TISSUE-BRAIN;			
RA	MEDLINE; 95161080.			
RT	CROSIER K.E., HALL L.R., LEWIS P.M., MORRIS C.M., WOOD C.R.,			
RL	MORRIS J.C., CROSIER P.S.;			
RP	"Isolation and characterization of the human DTK receptor tyrosine			
RL	kinase."			
RN	Growth Factors 11:137-144(1994).			
RP	SEQUENCE OF 519-720 FROM N.A.			
RX	MEDLINE; 94085793.			
RA	POLVI A., ARMSTRONG E., LAI C., LENKE G., HUBNER K., SPRITZ R.A.,			
RT	GIUDA L.C., NICHOLS R.D., ALITALO K.;			
RL	"The human TYRO3 gene and pseudogene are located in chromosome			
RP	15q11-q25."			
RN	Gene 134:289-293(1993).			
CC	- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY			
CC	IN THE CENTRAL NERVOUS SYSTEM.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN			
CC	OTHER TISSUES.			
CC	- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC			
CC	DOMAIN.			
CC	- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
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CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/			
CC	or send an email to license@isb-sdb.ch).			
DR	EMBL; U05682; AAA19236.1; -			
DR	EMBL; D17517; BAA04467.1; -			
DR	EMBL; U18934; AAC50070.1; -			

44 534.5 11.4 1182 1 ABL2_HUMAN P42684 homo sapien
45 533.5 11.4 1607 1 MIPR_LYMSM Q25410 lymnaea sta

Query Match	Similarity	Score	DB 1	Length
Best Local	96.1%	2403	DB 1	890
Matches	467	Conservative	4	Mismatches 15; Indels 0; Gaps 0
QY	382	FSQOMADSTFESVVOQONSNPAMRAWPVYLVLTALYTAALALILTKRKREKREFOAF	441	
DB	405	WSQGLVYSSHDRAQGOOGPHSRKSWPVVVLGVLTALYTAALALILTKRKREKREFOAF	464	
QY	442	DSVWARGEPVNHRAARSEFNREPERIEATLTDLSLSDLEKLEKEDVLIPEOQFTTGRML	501	
DB	465	DSVWARGEPVNHRAARSEFNREPERIEATLTDLSLSDLEKLEKEDVLIPEOQFTTGRML	524	
QY	502	GKGFGSVRAQOLKQEDGSFVYAVYAKMLADIASSDIEEFLRPAACKKEFDHPHAKVLY	561	
DB	525	GKGFGSVRAQOLKQEDGSFVYAVYAKMLADIASSDIEEFLRPAACKKEFDHPHAKVLY	584	
QY	562	GVSLRSARAKRLPIPVILLPEMKHGDIAFLASLIGENPNPLQTLIRFMDIACGME	621	
DB	585	GVSLRSARAKRLPIPVILLPEMKHGDIAFLASLIGENPNPLQTLIRFMDIACGME	644	
QY	622	YLSRNFIRHEDLAARNCMLAEDMTVCVADFGLSRKITYGDDYRQGCASKIPVYMLAESI	681	
DB	645	YLSRNFIRHEDLAARNCMLAEDMTVCVADFGLSRKITYGDDYRQGCASKIPVYMLAESI	704	
QY	682	ADNULYVQSDYMAFGVYTMELINTRGQTPYAGIENNAEINYVLIGNRLLKQPECEMEDYDL	741	
DB	705	ADNULYVQSDYMAFGVYTMELINTRGQTPYAGIENNAEINYVLIGNRLLKQPECEMEDYDL	764	
QY	742	MYQMSADPQRPQSFCLRMELNLTIGQLSVLSAQDPLYNINRAEPPAGSGLELPGR	801	
DB	765	MYQMSADPQRPQSFCLRMELNLTIGQLSVLSAQDPLYNINRAEPPAGSGLELPGR	824	
QY	802	DQPYSGAGDSGAGVGTPTSDCRYILTPGGLAEQPGQAHEQSPSPNETORILLQOQGI	861	
DB	825	DQPYSGAGDSGAGVGTPTSDCRYILTPGGLAEQPGQAHEQSPSPNETORILLQOQGI	884	

OY	862	LPHSSC	867
DB	885	LPHSSC	890
RESULT 2			
ID	TYR3_RAT	STANDARD:	PRT: 880 AA.
AC	P55146.		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUL-1999 (Rel. 39, Last annotation update)		
DE	TYROSINE-PROTEIN KINASE RECEPTOR TYR03 PRECURSOR (TYROSINE-PROTEIN KINASE SKI).		
GN	TYR03 OR SKI.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RX	TISSUE-BRAIN:		
RX	MEDLINE; 96104999.		
RA	OHASHI K., HONDA S., ICHINOYA N., NAKAMURA T., MIZUNO K.;		
RT	"Molecular cloning and in situ localization in the brain of rat ski receptor tyrosine kinase.";		
RL	J. Biochem. 117:1267-1275(1995).		
CC	- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY IN THE CENTRAL NERVOUS SYSTEM.		
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN OTHER TISSUES.		
CC	- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN.		
CC	- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.		
CC	- SIMILARITY: CONTAINS 2 FIBROECTIN TYPE III-LIKE DOMAINS.		
CC	-----		
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CC	-----		
DR	EMBL; D37880; BAA07119.1; ..		
DR	HSSP; P1362; IEG1.		
DR	PFAM; PF00041; fn3; 2.		
DR	PFAM; PF00047; fn3; 2.		
DR	PFAM; PF00069; pkinase; 1.		
DR	PROSITE; PS0107; PROTEIN_KINASE_ATP_1.		
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR_1.		
DR	PROSITE; PSS0011; PROTEIN_KINASE_DOM_1.		
KW	Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transmembrane; Phosphorylation; Signal; Repeat; Immunoglobulin domain.		
FT	SIGNAL	1	30
FT	CHAIN	31	880
FT	DOMAIN	31	419
FT	TRANSSEM	420	440
FT	DOMAIN	441	880
FT	DOMAIN	34	115
FT	DOMAIN	131	200
FT	DOMAIN	214	301
FT	DOMAIN	305	401
FT	DOMAIN	508	785
FT	NP_BIND	514	522
FT	BINDING	540	540
FT	ACT_SITE	645	645
FT	MOD_RES	676	676
FT	CARBHYD	53	53
FT	CARBHYD	75	75
FT	CARBHYD	181	181
FT	POTENTIAL.		
FT	TYROSINE-PROTEIN KINASE RECEPTOR TYR03.		
FT	EXTRACELLULAR (POTENTIAL).		
FT	POTENTIAL.		
FT	CYTOPLASMIC (POTENTIAL).		
FT	IG-LIKE DOMAIN.		
FT	IG-LIKE DOMAIN.		
FT	FIBONECTIN TYPE-III.		
FT	FIBONECTIN TYPE-III.		
FT	PROTEIN_KINASE.		
FT	ATP (BY SIMILARITY).		
FT	AAP (BY SIMILARITY).		
FT	BY SIMILARITY.		
FT	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).		
FT	POTENTIAL.		
FT	POTENTIAL.		
FT	POTENTIAL.		

ID	TYRO3_MOUSE	STANDARD;	PRT;	880 AA.
P55144;				
01-OCT-1996	(Rel. 34, Created)			
01-OCT-1996	(Rel. 34, last sequence update)			
15-JUL-1999	(Rel. 38, last annotation update)			
TYROSINE-PROTEIN KINASE RECEPTOR TYROS	PRECURSOR (TYROSINE-PROTEIN			
KINASE RSE) (TYROSINE-PROTEIN KINASE DTK)	(TK19-2).			
TYRO3 OR DTK OR RSE.				
Mus musculus (Mouse).				
Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.				
[1]				
SEQUENCE FROM N.A.				
TISSUE-BRAIN:				
MEDLINE: 94193774.				
MAR M.R., SCADDEN D.T., WANG Z., GU Q., GODDARD A., GODOWSKI P.J.;				
RSE, a novel receptor-type tyrosine kinase with homology to AxL/Ufo,				
is expressed at high levels in the brain.";				
J. Biol. Chem. 269:10720-10728(1994).				
[2]				
SEQUENCE FROM N.A.				
TISSUE-BRAIN:				

RX	MEDLINE: 95161079.	
RA	CROSIER P.S., LEWIS P.M., HALL L.R., VITAS M.R., MORRIS C.M.,	
RA	BELER D.R., WOOD C.B., CROSIER K.E.;	
RT	"Isolation of a receptor tyrosine kinase (PTK) from embryonic stem	
RT	cells: structure, genetic mapping and analysis of expression.";	
RL	Growth Factors 11:125-136(1994).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-C57BL/6;	
RX	MEDLINE: 94336210.	
RT	LAI C., GORE M., LENKE G.;	
RT	"Structure, expression, and activity of Tyro 3, a neural adhesion-	
RT	related receptor tyrosine kinase.";	
RL	Oncogene 9:2567-2578(1994).	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-BALB/C; TISSUE-BRAIN;	
RX	MEDLINE: 95240399.	
RA	SCHULZ N., PAULHIC C., LEE L., ZHOU R.;	
RT	"Isolation and expression analysis of tyro3, a murine growth factor	
RT	receptor tyrosine kinase preferentially expressed in adult brain.";	
RL	Brain Res. Mol. Brain Res. 28:273-280(1995).	
RN	[5]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-BALB/C; TISSUE-BRAIN;	
RA	SASAKI M.;	
RL	Submitted (JUN-1995) to the EMBL/genbank/DBJ databases.	
CC	-1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY	
CC	IN THE CENTRAL NERVOUS SYSTEM.	
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-1- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN	
CC	OTHER TISSUES.	
CC	-1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC	
CC	DOMAIN.	
CC	-1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.	
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.	
CC	-----	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/isb-sib.ch).	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL: U05683; AAA19237.1; .	
DR	EMBL: UI8933; AAC52148.1; .	
DR	EMBL: X78103; CA854995.1; ALT_INIT.	
DR	EMBL: UI8342; AAB26942.1; ALT_INIT.	
DR	EMBL: AB000828; BAA19193.1; .	
DR	HSSP: P11362; IFGI.	
DR	MGD: MG1:104294; TYRO3.	
DR	Pfam: PF00041; fn3.2.	
DR	Pfam: PF00047; Ig; 2.	
DR	Pfam: PF00059; pkinase.1.	
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP.1.	
DR	PROSITE: PS00109; PROTEIN_KINASE_TYR.1.	
DR	PROSITE: PSS0011; PROTEIN_KINASE_DOM.1.	
KW	Receptor; Glycoprotein; Tyrosine protein kinase; ATP-binding;	
KW	Transferrin; Phosphorylation; Transmembrane; Signal; Repeat;	
KW	Immunoglobulin domain.	
FT	SIGNAL	POTENTIAL.
FT	CHAIN	TYROSINE-PROTEIN KINASE RECEPTOR TYRO3.
FT	DOMAIN	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	PORECELLULAR (POTENTIAL).
FT	DOMAIN	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	IG-LIKE DOMAIN.
FT	DOMAIN	IG-LIKE DOMAIN.
FT	DOMAIN	FIBRONECTIN TYPE-II.
FT	DOMAIN	FIBRONECTIN TYPE-III.
FT	DOMAIN	FIBRONECTIN TYPE-III.
FT	DOMAIN	PROTEIN KINASE.
FT	NP_BIND	ATP (BY SIMILARITY).
FT	ND_BIND	ATP (BY SIMILARITY).
FT	BINDING	ATP (BY SIMILARITY).

RA	RESULT	4	UFO_HUMAN	ID	UFO_HUMAN	STANDARD;	PRT;	887	AA.
AC				P30530.					
DI				01-APR-1993	(Rel. 25, Created)				
DT				01-APR-1993	(Rel. 25, Last sequence update)				
DT				15-JUL-1999	(Rel. 38, Last annotation update)				
DE				TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE).					
GN				AXL OR UFO.					
OS				Homo sapiens (Human).					
OC				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;					
OC				Eutheria; Primates; Catarrhini; Homnidae; Homo.					
RN				[1]					
RP				SEQUENCE FROM N.A.					
RX				MEDLINE: 92050809.					
RA				JANSSEN J.W.G., SCHULZ A.S., STEENVOORDEN A.C.M., SCHMIDBERGER M.,					

Query Match	25.7%;	Score 1200.5;	DB 1;	Length 887
Best Local Similarity	51.1%;	Pred. No. 6.4e-67;		

Matches 243; Conservative 72; Mismatches 132; Indels 29; Gaps 9;

QY 386 WADSTFSVYQ--ONSNA--WRAVPEVVLGVLTALYTAALALILKRRKRRKRFQCA 440
 DB 419 WRPEADPQHVLTKEPSPAPSPMWMY-VLLGAVYAAACVLLALFLVHRKRRKRYGEV 477
 QY 441 FDSVMANGEPVHRAARSFRERPERLEATLDSIGIDELKEKEDVLLPEQOFTLGRM 500
 DB 478 FEPTVEGELVVRVRYSR---RTTEATLNSIGISEEKELRDVVRHKKVALGKT 534
 QY 501 LGKGEFSVREAOIKOEDGSFVYAVKMLKADITASSDIEFLRAACMKREDPHVAKL 560
 DB 535 LGSEEPFVAVGQANOD-SILKVAVTKMKAICTRSELEFLSAVCKMKEFDHPVRL 593
 QY 561 VGVLSRANGRLPIPVILPFMKHGLHAFLASRIGENFNLPLQTLIRFVADIGM 620
 DB 594 IGVOFOSERESFPAPVILPEFMKRGDLSLRSLOGOVYLPQMLVFMADISGM 653
 DB 621 EYLSRNFIRDLAARCMKAEDMTVCVADFGLSRKIYSGDYRQGCASKLPMKLALES 680
 DB 654 EYLSKRFIRDLAARCMKNENMSCVADFGLSRKIYNGDYRGRKAKKPMKIAIES 713
 QY 681 LADNLVYQSDVMAFGVTMEIRGQTPVAGIEMAEYNYLIGGNLAKOPCEMEDYD 740
 DB 714 LADRVYTSKSDVMSFGVTMEIATRGQTPGVENSEYDYLROGNRLKOPADLDGLYA 773
 QY 741 LMYQCSADPKRPSFTCLMELNENIGQLSVLSASODPLYINIERA---EETPAGSL 796
 DB 774 LMSRCMELNPDQSPSEFLNEDLENTKALPRAOPPEILYVNDDEGGCPPEPGAAAGA 833
 QY 797 ELFGROPYISGAGDGSMAVGGTPSDCRILTPG-----GLAEPQGA 841
 DB 834 DPPTOPDPKDC--SCLTAAEVHAG-RVYLCPTSPAPQADRSAPAGED 885

RESULT 5
 UFO_MOUSE STANDARD; PRT; 888 AA.

AC 000993;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112)
 DE (ADHESION-RELATED KINASE).
 GN UFO OR ARK.
 MS Mus. musculus (Mouse).
 MS Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 MS Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1; TISSUE-HEART;
 RX MEDLINE: 92319537.
 RA FAUST M., EBENSPEGER C., SCHULZ A.S., SCHLETHOFF L., HAMEISTER H.,
 RA BARTRAM C.R., JANSSEN J.W.G.;
 RA "The murine ufo receptor: molecular cloning, chromosomal localization
 and in situ expression analysis.";
 RL Oncogene 7:1287-1293(1992).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 9201811.
 RA RESCIGNO J., MANSUKHANI A., BASILICO C.;
 RA "A putative receptor tyrosine kinase with unique structural
 topology.";
 RL Oncogene 6:1909-1913(1991).
 CC -1- FUNCTION: MAY FUNCTION AS A SIGNAL TRANSDUCER BETWEEN SPECIFIC
 CC -1- CELL TYPES OF MESODERMAL ORIGIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: IN DISTINCT SUBSTRUCTURES OF A BROAD SPECTRUM
 CC OF DEVELOPING TISSUES (IN THE LATE EMBRYOGENESIS). IN CELLS
 CC FORMING ORGAN CAPSULES AS WELL AS IN CONNECTIVE TISSUE STRUCTURES
 CC (IN ADULT).
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN.

CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 803
 CC ONWARD DUE TO A FRAMESHIFT.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X63535; CAA45097.1; -
 DR EMBL: X59560; CAA2158.1; ALT_FRAME.
 DR PIR: S23065; S23065.
 DR PIR: S23251; S23251.
 DR HSP: P11362; IFGI.
 DR MGD: MGI:98896; UFO.
 DR PAM: PF00041; fn3. 2.
 DR PAM: PF00047; 1g. 2.
 DR PAM: PF00069; PKinase. 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR. 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
 KW Transferase; Phosphorylation; Transmembrane; Signal; Repeat;
 KW Immunoglobulin domain.
 FT SIGNAL 1 18
 FT CHAIN 19 888
 FT DOMAIN 19 443
 FT TRANSMEM 444 466
 FT DOMAIN 467 888
 FT DOMAIN 30 119
 FT DOMAIN 135 206
 FT DOMAIN 218 316
 FT DOMAIN 320 417
 FT DOMAIN 530 801
 FT NP_BIND 536 544
 FT BINDING 561 561
 FT ACT_SITE 666 666
 FT MOD_RES 697 697
 FT CARBOHYD 37 37
 FT CARBOHYD 151 151
 FT CARBOHYD 192 192
 FT CARBOHYD 333 333
 FT CARBOHYD 339 339
 FT CARBOHYD 395 395
 FT CONFLICT 30 45
 FT CONFLICT 69 70
 FT CONFLICT 277 286
 FT CONFLICT 394 394
 FT CONFLICT 486 486
 FT CONFLICT 566 566
 FT CONFLICT 698 699
 FT CONFLICT 728 728
 FT CONFLICT 758 758
 FT CONFLICT 768 768
 FT CONFLICT 774 774
 FT CONFLICT 774 774
 SQ SEQUENCE 888 AA; 98251 MW; 00378693 CRC32;
 IL -> MV (IN REF. 2).
 ILTVQSVDPH -> PHASISAP (IN REF. 2).
 A -> R (IN REF. 2).
 G -> P (IN REF. 2).
 A -> V (IN REF. 2).
 HQ -> AK (IN REF. 2).
 S -> L (IN REF. 2).
 Q -> K (IN REF. 2).
 F -> C (IN REF. 2).
 S -> A (IN REF. 2).
 Query Match 25.2%; Score 1178.5; DB 1; Length 888;
 Best Local Similarity 51.3%; Pred. No. 1.5e-65;
 Matches 237; Conservative 69; Mismatches 129; Indels 27; Gaps 6;

QY 399 SRAPARA-----WVAVLVLTALYTAALALILKRRKRRKRGAFDSVARGEPAYHF 454
 DB 433 SEPPRAFSWPMYVLLALYAAACVLLALFLVHRKRRKRYGEVFEPTVEGELVVR 492
 QY 455 RAARSFNRERPERIATLDSIGIDELKEKEDVLLPEQOFTLGRMKGFGSVREQL 514

Db 493 RYKSYR---RTTEATLNSLGISEELKEKLRVMDRHKVALGKLGEGEFAVNEGOL 549
 QY 515 KODGSEFVAVYAKMLADIASDIEEFLREAAKMEFDPHVAKLGVSLSRANKRLP 574
 Db 550 MODD-SILKVAATKMTALICTRSELEDFLEAVCKEFDHPNMRLLIGVCGSDREGPP 608
 QY 575 IPWVILPEPMKHGDLHAFLASRIGENPNPLPOTLIRFVNDICGMEYLSRNFIRDLA 634
 Db 609 EPVVLPEPMKHGDLHAFLASRIGENPNPLPOTLIRFVNDICGMEYLSRNFIRDLA 668
 QY 635 ARNCMLAEDMTVCVADFGLSRKIYSGDYRQGCASKLPMKWLALSLADNLTYSQSDVA 694
 Db 669 ARNCMLNENNSVCVADFGLSRKIYSGDYRQGCASKLPMKWLALSLADNLTYSQSDVA 728
 QY 695 FGVTMWEITRGOTPYAGIENAEIYVLYLGNLKPQPCMEDVDYDMYOCMSADPKORP 754
 Db 729 FGVTMWEITRGOTPYAGIENAEIYVLYLGNLKPQPCMEDVDYDMYOCMSADPKORP 788
 QY 755 SFCLMELNLTIGOLSVLASODPLYXINIERA-----EPTAGSGSELGROQFISGAGD 810
 Db 789 SFCLMELNLTIGOLSVLASODPLYXINIERA-----EPTAGSGSELGROQFISGAGD 844
 Db 811 GSGMAGVGTSPDCRYILTPG-----GLAEQPGCAE 841
 Db 845 SCSCFLAADVHAGRYVLCPTAPGPTLSADRCGAPRQGED 886

RESULT 6

RRK_AVIR3 STANDARD; PRT: 442 AA.
 AC P33497;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN RYK (EC 2.7.1.112).
 GN V-RYK.
 OS Avian retrovirus RPL30.
 OC Viruses; Retroviridae; Avian type C retroviruses.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92407992.
 RA JIA R., MAYER B.J., HANAFUSA T., HANAFUSA H.;
 RT "A novel oncogene, v-ryk, encoding a truncated receptor tyrosine
 RT kinase is transduced into the RPL30 virus without loss of viral
 RT sequences."
 RL J. Virol. 66:5975-5987(1992).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: CELL MEMBRANE.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A ENV-RYK
 CC POLYPEPTIDE. AN ENV-RYK PRECURSOR FUSION PROTEIN IS FIRST
 CC SYNTHESIZED AND THEN CELLULAR PROTEASE CLEAVES THIS PRECURSOR INTO
 CC GP85 AND THE PUTATIVE ONCOGENE TERMED GP87(RYK).
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN.
 CC -----
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC EMBL; M92847; AAA42673.1;
 DR PIR; B43362; B43362.
 DR HSSP; P11362; 1RG1.
 DR PFAM; PF00069; PKINASE.1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR.1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM.1.
 KW Polypeptide; Transforming protein; Tyrosine-protein kinase;
 KW Transferase; Phosphorylation; ATP-binding; Oncogene; Membrane.

FT DOMAIN 45 316 PROTEIN KINASE.
 FT NP_BIND 51 59 ATP (BY SIMILARITY).
 FT BINDING 77 77 ATP (BY SIMILARITY).
 FT ACT_SITE 181 181 BY SIMILARITY.
 FT MOD_RES 212 212 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 442 AA; 49108 MW; 24FD246D CRC32;

Query Match 22.7%; Score 1061.5; DB 1; Length 442;
 Best Local Similarity 49.4%; Pred. No. 1,1e-58;
 Matches 217; Conservative 72; Mismatches 125; Indels 25; Gaps 6;

QY 452 VERRARSEFNERPERIATLSDIGISDELKEKEDVLIPEQOFLGMLGKGEFSGVRE 511
 Db 5 VVYTAKKSYCR---RAVELTSLGSLVSESLQKQDDVIDRNLALSLGVYLGEGEYSWE 61
 QY 512 AOLKEDDSFVAVYAKMLADIASDIEEFLREAAKMEFDPHVAKLGVSLSRANK 571
 Db 62 GRLSQPEGTPOKVAATKMTALICTRSELEDFLEAVCKEFDHPNMRLLIGVCG 121
 QY 572 RLPIWVILPEPMKHGDLHAFLASRIGENPNPLPOTLIRFVNDICGMEYLSRNF 631
 Db 121 QIPKRVVLPFKMGYDLSFLRSKLENAPOFVPLQMLKTRVNDIALGMEYLSRQFL 180
 QY 632 DLAAKNCMLAEDMTVCVADFGLSRKIYSGDYRQGCASKLPMKWLALSLADNLT 691
 Db 181 DLAAKNCMLAEDMTVCVADFGLSRKIYSGDYRQGCASKLPMKWLALSLADNLT 240
 QY 692 VVARGVMTWEITRGOTPYAGIENAEIYVLYLGNLKPQPCMEDVDYDMYOCMSAD 751
 Db 241 VVARGVMTWEITRGOTPYAGIENAEIYVLYLGNLKPQPCMEDVDYDMYOCMSAD 300
 QY 752 QRPSTFCMLNLTIGOLSVLASODPLYXINIERA-----PRAGSLE 797
 Db 301 DRPFSQAKVLEKLESLPAPRSGSKDYIVNTSLPESPSTQDLGDSYTPQDSDLD 360
 QY 798 LPRGDPYSGAGSGMAGVGTSPDCRYILTPGGLAEQPGCAEHQSPPLNETORLL 857
 Db 361 -PGDIAEPCCSHTKAAVAVDIHOGSKRYVLESG---SPEDNAVVPQLP---HEGSAMT 413
 QY 858 OQGLPFSKCAASLAKMD 876
 Db 414 EASTLPVGSSLAQLPCAD 432

RESULT 7

SEA_AVIR3 STANDARD; PRT: 370 AA.
 AC P23049;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SEA (EC 2.7.1.112).
 GN V-SEA.
 OS Avian erythroblastosis virus (strain 513).
 OC Viruses; Retroviridae; Avian type C retroviruses.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89315783.
 RA SMITH D.R., VOGT P.K., HAYMAN M.J.;
 RT "The v-sea oncogene of avian erythroblastosis retrovirus 513: another
 RT member of the protein-tyrosine kinase gene family."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5291-5295(1989).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A ENV-SEA
 CC POLYPEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE MET TYROSINE KINASE FAMILY OF RECEPTOR.
 CC -----
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CC EMBL; M25158; E14458; -

DR PIR; B33902; TVEVSA.

DR HSSP; P11362; 1FGI.

DR PFAM; PF00069; PKinase; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TPR; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR Polypeptide; Transforming protein; Tyrosine-protein kinase; ATP-binding; Oncogene; Phosphorylation.

FT DOMAIN 60 323 PROTEIN KINASE.

FT NP_BIND 66 74 ATP (BY SIMILARITY).

FT BINDING 92 92 ATP (BY SIMILARITY).

FT ACT_SITE 186 186 BY SIMILARITY.

FT MOD_RES 216 216 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT SEQUENCE 370 AA; 41701 MW; P2E82A14 CRC32;

Query Match 13.8%; Score 646; DB 1; Length 370;

Best Local Similarity 40.3%; Pred. No. 3.8e-33;

Matches 144; Conservative 58; Mismatches 121; Indels 34; Gaps 9;

QY 432 RKEFRQADSVARREPAVHFAANSFNERPERLEATISGIDELKEDVLP 491

DB 8 RPAHFASAGADAGGSPVLLRTT-----SCLEDD--RELEEVKIDILIP 54

QY 492 EEOFTL--GNMLKGEFVSREALQKEDGSFVAVYAKMKAQDIASDIEFREAACM 549

DB 55 EELILTRSRVIGHGHSYHYGTMDPLGLNLCVAKSLR--TYLEEVFEFLREGILM 113

QY 550 KEEDHPVAVIVGYSLSRSRAGRLPIPVILPEFKHGDILHAFLASRIGEPFPLQTL 609

DB 114 KGFHHQVYLLGLCL-----PRHGLPLVLPYHRHGDILHFAVAGQ--RSP---TYKEL 163

QY 610 IRPWVDAICMEYISNFTHRDLAARNCMLAEDMYCVADFGLSRTYSGDY--RQGC 667

DB 164 IGFGLVYALCMEXYLAQKFKFHRDLAARNCMLDELITVYVADFGIARVDFGKEYYSINQHR 223

QY 668 ASLTPVYKALLESADLYVOSDYNAPGVYMEIMRGCPFYAGIENALYINLIGNR 727

DB 224 HALLPVYKMLLESIQTKFTKSDVMSFVYVWELLRGASPYEVDPYDARLLGRR 283

QY 728 LKQPFCEMEDVDYLMYOCWSADPKRPSFTCLRMELNIIIGOLSVLASODPLXINI 784

DB 284 LPQPOCPDPLVGVMLSCWAPTEPERPSFGVGLCELRVLAFL-----EGEYIIM 334

RESULT 8

MET_MOUSE STANDARD: PRT: 1379 AA.

AC P16056; 062125; (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-APR-1990 (Rel. 14, Last annotation update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE HEPATOCYTE GROWTH FACTOR RECEPTOR PRECURSOR (MET PROTO-ONCOGENE TYROSINE KINASE) (EC 2.7.1.112) (HGF-SF RECEPTOR).

GN MET.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC (1)

RP SEQUENCE FROM N.A.

RX MEDLINE; 88262253.

RA CHAN A.M.L., KING H.W.S., DEAKIN E.A., TEMPEST P.R., HIKKENS J., KROELEN V., EDWARDS D.R., WILLS A.J., BROOKES P., COOPER C.S.; "Characterization of the mouse met proto-oncogene."

RT Oncogene 2:593-599(1988).

RN (2)

RP SEQUENCE OF 1199-1270 FROM N.A.

RX MEDLINE; 90152381.

RA WILKS A.F., KURBAN R.R., HOVENS C.M., RALPH S.J.; "The application of the polymerase chain reaction to cloning members of the protein tyrosine kinase family."

RT Gene 85:67-74(1989).

RL Gene 85:67-74(1989).

CC -1- FUNCTION: RECEPTOR FOR HEPATOCYTE GROWTH FACTOR. HAS A TYROSINE-PROTEIN KINASE ACTIVITY.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBUNIT: HETERODIMER FORMED OF AN ALPHA CHAIN (50 KD) AND A BETA CHAIN (45 KD) WHICH ARE DISULFIDE LINKED.

CC -1- STRUCTURAL LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- DISEASE: ACTIVATION OF MET AFTER REARRANGEMENT WITH THE TPR (TRANSLOCATED PROMOTER) LOCUS OF CHROMOSOME 1 PRODUCES AN ONCOGENIC PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE MET TYROSINE KINASE FAMILY OF RECEPTOR.

CC -----

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CC -----

DR EMBL; Y00671; CAA68680.1; -

DR EMBL; M33424; AAA40015.1; -

DR PIR; S01254; S01254.

DR HSSP; P11362; 1FGI.

DR MCD; MGI:96869; MET.

DR PFAM; PF00069; PKinase; 1.

DR PFAM; PF01437; Plexin_repeat; 1.

DR PFAM; PF01437; Plexin_repeat; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TPR; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR Transferrase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding; K W Receptor; Transmembrane; Glycoprotein; Phosphorylation; Signal.

FT SIGNAL 1 24

FT CHAIN 25 1379

FT DOMAIN 25 931

FT TRANSMEM 932 954

FT DOMAIN 955 1379

FT DOMAIN 1076 1343

FT SITE 306 307

FT NE_BIND 1082 1090

FT BINDING 1108 1108

FT ACT_SITE 1202 1202

FT MOD_RES 1233 1233

FT CARBOHYD 45 45

FT CARBOHYD 106 106

FT CARBOHYD 201 201

FT CARBOHYD 357 357

FT CARBOHYD 398 398

FT CARBOHYD 404 404

FT CARBOHYD 606 606

FT CARBOHYD 634 634

FT CARBOHYD 784 784

FT CARBOHYD 878 878

FT CONFLICT 1159 1159

FT CONFLICT 1255 1255

FT CONFLICT 1261 1261

FT CONFLICT 1269 1270

SO SEQUENCE 1379 AA; 153548 MW; E1597F1A CRC32;

Query Match 13.2%; Score 615.5; DB 1; Length 1379;

Best Local Similarity 31.7%; Pred. No. 1.3e-30;

Matches 171; Conservative 80; Mismatches 177; Indels 111; Gaps 21;

QY 348 GNTQDECEQLERFSQNPCLVETAIKAFHQLFSQVADSTFS-----VYQQNSNPA 402

DB 877 GN--QSCESLHWHSAGVAVICTVPSDLKLKLNSEINI---EKQAVSVYSLGKVIYVDPDON-- 930


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RP IDENTIFICATION OF FN-III REPEATS.
RX MEDLINE; 9019889.
RX NORTON P.A., HYNES R.O., RESS D.J.G.;
RT "Sevenless: seven found?";
RL Cell 61:15-16(1990).
CC -1- FUNCTION: RECEPTOR FOR AN EXTRACELLULAR SIGNAL REQUIRED TO
CC INSTRUCT A CELL TO DIFFERENTIATE INTO A R7 PHOTORECEPTOR. THE
CC LIGAND FOR SEV IS THE BOSS (BRIDE OF SEVENTEEN) PROTEIN ON THE
CC SURFACE OF THE NEIGHBORING R8 CELL.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBUNIT: MAY FORM A COMPLEX WITH DRK AND SOS.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. SEVENTEENLESS SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 7 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -1- CAUTION: UNCLEAR WHETHER THE POTENTIAL MEMBRANE SPANNING REGION
CC NEAR THE N-TERMINUS IS PRESENT AS A TRANSMEMBRANE DOMAIN IN THE
CC NATIVE PROTEIN OR SERVES AS A CLEAVED SIGNAL SEQUENCE.
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CC -----
DR EMBL; X13666; CAA13960.1; ALT_INT.
DR EMBL; J03158; AAA28882.1; -.
DR PIR; A28912; TYEPTL.
DR HSSP; P11362; 1FG1.
DR FLYBASE; F8gn0003366; sev.
DR PFM; PFO0041; fn3; 6.
DR PFM; PFO0069; pkinaase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW transferase; tyrosine-protein kinase; transmembrane; ATP-Binding;
KW Phosphorylation; Receptor; Vision; Repeat.
KW DOMAIN 1 2123 EXTRACELLULAR (POTENTIAL)

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FT	TRANSMEM	2144	2147	POTENTIAL.
FT	DOMAIN	2148	2554	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	311	431	FIBRONECTIN TYPE-III.
FT	DOMAIN	436	528	FIBRONECTIN TYPE-III.
FT	DOMAIN	822	921	FIBRONECTIN TYPE-III.
FT	DOMAIN	1298	1392	FIBRONECTIN TYPE-III.
FT	DOMAIN	1680	1794	FIBRONECTIN TYPE-III.
FT	DOMAIN	1797	1897	FIBRONECTIN TYPE-III.
FT	DOMAIN	1898	1988	FIBRONECTIN TYPE-III.
FT	DOMAIN	2038	2046	POLY-ARG.
FT	DOMAIN	2209	2485	PROTEIN KINASE.
FT	NP_BIND	2215	2223	ATP (BY SIMILARITY).
FT	BINDING	2242	2242	ATP (BY SIMILARITY).
FT	MUTAGEN	2242	2242	K-M: INACTIVATES THE PROTEIN.
FT	MOD. RES	2380	2380	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	CARBOHYD	30	30	POTENTIAL.
FT	CARBOHYD	129	129	POTENTIAL.
FT	CARBOHYD	481	481	POTENTIAL.
FT	CARBOHYD	505	505	POTENTIAL.
FT	CARBOHYD	617	617	POTENTIAL.
FT	CARBOHYD	647	647	POTENTIAL.
FT	CARBOHYD	966	966	POTENTIAL.
FT	CARBOHYD	1228	1228	POTENTIAL.
FT	CARBOHYD	1313	1313	POTENTIAL.
FT	CARBOHYD	1353	1353	POTENTIAL.
FT	CARBOHYD	1550	1550	POTENTIAL.
FT	CARBOHYD	1557	1557	POTENTIAL.
FT	CARBOHYD	1639	1639	POTENTIAL.
FT	CARBOHYD	1725	1725	POTENTIAL.
FT	CARBOHYD	1756	1756	POTENTIAL.
FT	CARBOHYD	1804	1804	POTENTIAL.

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FT CAROHD 1889 1889 POTENTIAL.
FT CAROHD 1947 1947 POTENTIAL.
FT CAROHD 2073 2073 POTENTIAL.
FT VARIANT 392 392 M -> V.
FT VARIANT 1668 1668 N -> V.
FT VARIANT 1703 1703 N -> H.
FT VARIANT 1730 1730 G -> K.
FT VARIANT 1731 1731 G -> E.
FT VARIANT 1741 1741 V -> M.
FT VARIANT 2271 2271 R -> C.
FT CONFLICT 1823 1823 E -> Q (IN REF. 2).
SQ SEQUENCE 2554 AA; 267107 MW; 1143D891 CRC32;

Query Match 13.0% Score 610; DB 1; Length 2554;
Best Local Similarity 25.8%; Pred. No. 5.9e-30;
Matches 236; Conservative 106; Mismatches 313; Indels 260; Gaps 33;

QY 48 PVLDDLEGNL-----ATENFVNSCTQARKKCEANPACRAAYOHLSGSSSRP 100
1743 PLGQHLGAGESLNTDLLPFRYVSGILSFYOKIALPTLVLAPELTLASATPSPP 1802
QY 101 LPLESAMSADCLEA-----EQLRNSLIDCRHRMKHQATCLDIYMTVPARSLGYE 156
1803 RNFVSRLSPRELEVSMLPEOLRSES-----VYTLH-----WQOE 1839
QY 157 LDVSPYEDVTISKPMKMLSKLMLKPSDLCLKFMALCTLDKCDIRKAYGEGSGIR 216
1840 LDGENVQD-----RREWE-----AHER--RLFTAGTHLTIQK 1870
QY 217 CORHCLAGLSFFPKAKESHAQGLLPCPEPDAGCGER---RRNTAPSCALPSVTPN 273
1871 -----PSGSLWVOAH-----PPTKSNSEERLHVSFAELPELOLLELGPY 1913
QY 274 CLDLSFCRADPL-----CSRLLMDFOTHC---HPMDILGTCATEQSGRCRAVIGLIGT 324
1914 SLSLWACTPPLPLSGLOLECHSSAQLARRNVAAGNTKAVPELPRTYQCRLLIGIAT 1973
QY 335 AMTPNF-----ISKNVTVALSCTGSGS-----NL 350
1974 PGAPLYHGTAEYETLGDAPSGPKOLEHIAEVEFRTWIA-----RGNGAPIALYNL 2028
QY 351 Q-----DEGQLERSSONCLVEA 370
2029 EALQARSDIRRRRRRRNSGSLQELPWAEPVVEEDOMLDFCTTLLS-----CIYKS 2083
QY 371 IAAK-----MREHROLFSQDMA--DSTFSVOOQNSNPAMRAVYVGLVALATYAAALA 424
2084 LHSRLLEFRARSLENGMPYSESERVAPEPVSPKRSGLVALIATAPATVSSCYLA 2143
QY 425 LILKRRKRETRFGAOFDSVARGEPAAVFPAAFSFRERPERTEATLDSIGIDEL--- 482
2144 LVLVAKVQR-----RLNAKLLQOSRS--TMSNSTLQTOOQMAV 2184
QY 482 -----KELLED--VLIEP-----QOFTLGRMLGKGFSGSVRAOLKQEDGSF--VYAVAKML 529
2185 RNRAFSTTLSPADIALLPQIMWSQDKLRLFGSSGAFGEVYGQKTEDESEPOFAIKSL 2244
QY 530 KADIIASDIEFLREAAKKEFDHPHVAKLGVSLNSRAGRLPIPVATLPEKKHDLH 589
2245 RK-----GASEFELLQEOALMNFKNHENVRLVGLCFTDETS-----LINEHKEAGDL 2295
QY 590 AFLASRI-----GENFNLPLQTLIREMDIACGMEYLSSRNFIHDLAARNCLMAED- 644
2296 SYLRAARATSTOEPOPTAGLSELLELAWCIDVANGCSYLEDMHVRHDLACRNCLVTEST 2355
QY 644 -----MVCYVADFGLSKRTISGDIYRGCSKLPVKMLALESLADNLYTQSVYAFV 697
2356 GSTDRRRRTVKIGDFGLADITKSYTRKEGGLPVRMSPESLVDSGLFTQOSVYMAFGV 2415
QY 698 TMEIMTNGQTPYAGIENAEIYNLYLIGSNRLKOPPECMEDYDLMYOOWSADPKORSFT 757
2416 LCMELLTIGQOPVYAAARNFVLAHVKEGRLQPPKCTEKILYSLLLCNRIDPERSFR 2475

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QY 758 CLMELENI-----LGOLSVLASAD-----PLXINIERAPEPTAGSL- 797
2476 RCYMTLHISTDLARTQMASTADTVYSCSRPEKVFDFQPLEHNEHNPEDENITL 2535
QY 797 -ELPGRD-QPYSAG 809
2536 REVPLKDKOLYANEG 2550

RESULT 11
IGIR_BOVIN STANDARD; PRT; 640 AA.
ID IGIR_BOVIN STANDARD; PRT; 640 AA.
AC 005688;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112)
DE (FRAGMENT).
GN IGIR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX MEDLINE; 92119330.
RA SNEYERS M., KETTMANN R., MASSART S., RENAVILLE R., BURRY A.,
RA PORTETELLE D.;
RT Cloning and characterization of a cDNA encoding the beta-subunit of
RT the bovine insulin-like growth factor-1 receptor.;
RL DNA Seq. 1:405-406(1991)
CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
CC WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
CC TYROSINE-PROTEIN KINASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBUNIT: Tetramer of 2 alpha and 2 beta chains linked by disulfide
CC bonds. The alpha chains contribute to the formation of the ligand-
CC binding domain, while the beta chain carries the kinase domain.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
CC EMBL; X54980; CAA38724.1; -
CC HSSP; P06213; IIRK.
CC PRAM; PF00041; fn3.1.
CC PRAM; PF00069; pkinase.1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR.1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM.1.
CC PROSITE; PS00239; RECEPTOR_TYR_KIN_II.1.
CC Transferrase; Tyrosine-protein kinase; Receptor; Transmembrane;
CC Glycoprotein; ATP-binding; Phosphorylation; Repeat.
CC
CC CHAIN 1 13
CC CHAIN <1 13
CC CHAIN 14 640
CC CHAIN 14 640
CC DOMAIN 14 208
CC TRANSMEM 209 232
CC DOMAIN 233 640
CC DOMAIN <1 101
CC DOMAIN 101

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FT DOMAIN 102 201 FIBRONECTIN TYPE-III.
 FT 272 547 PROTEIN KINASE.
 FT NP_BIND 278 286 ATP (BY SIMILARITY).
 FT BINDING 306 306 ATP (BY SIMILARITY).
 FT ACT_SITE 408 408 BY SIMILARITY.
 FT MOD_RES 438 438 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 20 20 POTENTIAL.
 FT CARBOHYD 29 29 POTENTIAL.
 FT CARBOHYD 37 37 POTENTIAL.
 FT CARBOHYD 37 37 POTENTIAL.
 FT SEQUENCE 640 AA: 72511 MW: 72511 MD: FD7E7AF7 CRC32:

Query Match 13.08; Score 609.5; DB 1; Length 640;
 Best Local Similarity 28.28; Pred. No. 1.3e-30;
 Matches 170; Conservative 106; Mismatches 183; Indels 143; Gaps 22;

305 GSQVEDQREVSVROEYKKGAKLNINPGYTAHQAT-----SLSGNGS----- 189
 143 GSQVEDQREVSVROEYKKGAKLNINPGYTAHQAT-----SLSGNGS----- 189
 359 RSEFQNPCLVEAIAAKRFRHOLFSDMADSTFVVOQNSNPAMRAVPVVLGVLA-- 417
 189 -----WIDPVFFVQAKT-----YENFIHMLDPIAVL 218
 417 -LYTAALAILLKRKKRFRFGAEDSVNARCEPAVHFRANSEFNERERIEATIDSL 475
 219 LTVGLVIMLVFHRKRNSSRLG---NGVLVAVNPEYFSA----- 258
 476 GISDELKEKEDVLPE-----QOFTLGRMLGGEFGSGVREAOLK--QEDGSEYKAVK 527
 258 -----DYVPEDEWEVAREKITSRELQSGSGMYEGVAKVVDDEPTRAIK 306
 528 MKRADIIASSDIEEFLEAACKKEFDHPHAKLYGVLSRANKRGLPIPVYLPFMKGD 587
 307 TVN-EAASMERIEFLEAACKKEFDHPHAKLYGVLSRANKRGLPIPVYLPFMKGD 587
 588 LRAFL--LASRIGENPND-LQTLIRFVNDIACGMEYLSRNFIHRLAARCMLEAD 643
 360 LKSYLRLREPMENNPVLAAPSLSKMTQAGELADGWAYINANKFVRDLAARCMLEAD 419
 644 MNYCVADFGSKRTIGSDYRQGCASLTPYKMTALSLADNLTVOSDVNAFGVTMEIM 703
 420 FTVKIDFSGTIDYTDYRQGCASLTPYKMTALSLADNLTVOSDVNAFGVTMEIM 703
 704 TKGQFYAGIENAEIYNYLIGNRKOPRECMVDYDLMQCSADSKORPSF-----TCL 759
 480 TLAEPYQGLSNQVLRFTVEGGLDKPDKCPMTLELMKACQYKMKRPSFLEITISV 539
 760 RMELENIQLSVLSASQ-----DPLYINIERAE-----EPTA-GGSLLEPGRDQPSGA 808
 540 KDEMAGFREVSYSEENKPEPELEDELPEMMEVPLDPSASSASLPDR---HSGH 596
 809 GGSGGANGVGTSDCRITITPGGLAEQPOAHOEPSPIN---ETORLLLLQGLPLHS 865
 597 KAENGSG-----PGVLYLRASFDEROPRYAHNNGRKNERALPLPOS---S 638
 866 SC 867
 639 TC 640

RESULT 12
 MET_HUMAN STANDARD: PRT: 1390 AA.
 AC P08581:
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DT HEPATOCYTE GROWTH FACTOR RECEPTOR PRECURSOR (MET PROTO-ONCOGENE
 DE TYROSINE KINASE) (EC 2.7.1.112) (HGF-SF RECEPTOR).
 GN MET.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA GIORANDI S.;
 RL Submitted (NOV-1990) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87117655.
 RA PARK M.; DEAN M.; KAU K.; BRAUN M.J.; GONDA M.A.; VANDE WOUDE G.;
 RT "Sequence of MET proto-oncogene cDNA has features characteristic of
 the tyrosine kinase family of growth-factor receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6379-6383(1987).
 RN [3]
 RP SEQUENCE OF 1010-1390 FROM N.A.
 RX MEDLINE: 88143699.
 RA CHAN A.M.L.; KING H.W.S.; TEMPEST P.R.; DEAKIN E.A.; COOPER C.S.;
 RA BROOKES P.;
 RT "Primary structure of the met protein tyrosine kinase domain.";
 RL Oncogene 1:229-233(1987).
 RN [4]
 RP SEQUENCE OF 1206-1264 FROM N.A.
 RX MEDLINE: 94067791.
 RA LEE S.T.; STRUNK K.M.; SPRITZ R.A.;
 RT "A survey of protein tyrosine kinase mRNAs expressed in normal human
 melanocytes.";
 RL Oncogene 8:3403-3410(1993).
 RN [5]
 RP SEQUENCE OF 1267-1390 FROM N.A.
 RX MEDLINE: 86065462.
 RA DEAN M.; PARK M.; LE BEAU M.M.; ROBINS T.S.; DIAZ M.O.; ROWLEY J.D.;
 RA BLAIR D.G.; VANDE WOUDE G.F.;
 RT "The human met oncogene is related to the tyrosine kinase oncogenes.";
 RL Nature 318:385-388(1985).
 RN [6]
 RP SEQUENCE OF 1-754 FROM N.A.
 RA PAULEY A.; ANDREWS S.;
 RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP FUNCTION.
 RX MEDLINE: 91118019.
 RA BOTTARO D.P.; RUBIN J.S.; FALETTO D.L.; CHAN A.M.-L.; KMECIR T.E.;
 RA VANDE WOUDE G.F.; ARONSON S.A.;
 RT "Identification of the hepatocyte growth factor receptor as the c-met
 proto-oncogene product.";
 RL Science 251:802-804(1991).
 RN [8]
 RP PHOSPHORYLATION AT TYR-1235.
 RX MEDLINE: 92011756.
 RA FERRACINI R.; LONGATI P.; NALDINI L.; VIGNA E.; COMOGILIO P.M.;
 RT "Identification of the major autophosphorylation site of the
 met/hepatocyte growth factor receptor tyrosine kinase.";
 RL J. Biol. Chem. 266:19558-19564(1991).
 RN [9]
 RP VARIANTS HPRC, AND VARIANT VAL-320.
 RX MEDLINE: 97285124.
 RA SCHMIDT L.; DOH F.-M.; CHEN F.; KISHIDA T.; GLENN G.; CHOYKE P.;
 RA SCHERER S.N.; ZHANG Z.; LOBENSKY I.; DEAN M.; ALIKHETS R.;
 RA CHIDAMBARAM A.; BERGEREIM U.R.; FELTIS J.T.; CASADEVAL L.C.;
 RA ZAMARON A.; BERNDES M.; RICHARD S.; LIPS C.J.M.; WALTHER M.M.;
 RA TSUI L.-C.; GEIL L.; ORCUTT M.L.; STACKHOUSE T.; LIPAN J.; SLIFE L.;
 RA BRAUCH H.; DECKER J.; NIEHANS G.; HUGHSON M.D.; MOCH H.; STORKEL S.;
 RA LERMAN M.I.; LINEHAN W.M.; ZBAR B.;
 RT "Germline and somatic mutations in the tyrosine kinase domain of the
 met proto-oncogene in papillary renal carcinomas.";
 RL Nat. Genet. 16:68-73(1997).
 CC -1- FUNCTION: RECEPTOR FOR HEPATOCYTE GROWTH FACTOR. HAS A TYROSINE-
 PROTEIN KINASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
 PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBUNIT: HETERODIMER FORMED OF AN ALPHA CHAIN (50 KD) AND A BETA
 CHAIN (145 KD) WHICH ARE DISULFIDE LINKED.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DISEASE: ACTIVATION OF MET AFTER REARRANGEMENT WITH THE TPR

CC GENE PRODUCES AN ONCOGENIC PROTEIN.
 CC -1- DISEASE: DEFECTS IN MET ARE THE CAUSE OF HEREDITARY PAPILLARY
 CC RENAL CARCINOMA (HPRC). HPRC IS A FORM OF INHERITED KIDNEY CANCER
 CC CHARACTERIZED BY A PREDISPOSITION TO DEVELOP MULTIPLE, BILATERAL
 CC PAPILLARY RENAL TUMORS. THE PATTERN OF INHERITANCE IS CONSISTENT
 CC WITH AUTOSOMAL DOMINANT TRANSMISSION WITH REDUCED PENETRANCE.
 CC -1- SIMILARITY: BELONGS TO THE MET TYROSINE KINASE FAMILY OF RECEPTOR.
 CC
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 CC
 CC EMBL; M35074; AAA59590.1;
 CC EMBL; X54559; -; NOT_ANNOTATED_CDS.
 CC EMBL; J02958; AAA59591.1;
 CC EMBL; AC002080; AAB54047.1;
 CC PIR; A40175; TVEOME.
 CC HSP; P11362; 1FGI.
 CC MIM; 164860;
 CC PFAM; PF00069; PKinase; 1.
 CC PFAM; PF01403; Sema; 1.
 CC DR PFAM; PF01437; Plexin_repea; 1.
 CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC KW Transferrase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
 CC Receptor; Transmembrane; Glycoprotein; Phosphorylation; Signal;
 CC Chromosomal translocation; Disease mutation; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 1390
 FT DOMAIN 25 932
 FT TRANSMEM 933 955
 FT DOMAIN 956 1390
 FT NP_BIND 1078 1345
 FT BINDING 1104 1110
 FT ACT_SITE 1204 1204
 FT SITE 307 308
 FT SITE 1009 1010
 FT MOD_RES 1235 1235
 FT CARBOHYD 45 45
 FT CARBOHYD 106 106
 FT CARBOHYD 149 149
 FT CARBOHYD 202 202
 FT CARBOHYD 399 399
 FT CARBOHYD 405 405
 FT CARBOHYD 607 607
 FT CARBOHYD 635 635
 FT CARBOHYD 785 785
 FT CARBOHYD 879 879
 FT CARBOHYD 930 930
 FT CARBOHYD 930 930
 FT VARIANT 1131 1131
 FT VARIANT 1188 1188
 FT VARIANT 1195 1195
 FT VARIANT 1220 1220
 FT VARIANT 1228 1228
 FT VARIANT 1228 1228
 FT VARIANT 1230 1230
 FT VARIANT 1230 1230
 FT VARIANT 1230 1230

FT FT
 FT VARIANT 1250 1250 /FTID-VAR_006293.
 FT CONFLICT 755 755 M -> T (IN HPRC; SOMATIC MUTATION).
 FT CONFLICT 1191 1191 S -> STWKEPNTNITSELCFAS (IN REF. 2).
 SQ SEQUENCE 1390 AA; 15526 MW; 650992C2 CRC32;
 Query Match 13.0%; Score 606; DB 1; Length 1390;
 Best Local Similarity 40.1%; Pred. No. 5,2e-30; Mismatches 114; Indels 22; Gaps 7;
 Matches 129; Conservative 57;
 QY 472 LDSIGSDLEKKEKEDLVLEPQQFTL--GRLGKGEFVREAOLOKQDGSFVAVAKML 529
 DB 1053 IDLSALNPVLQAVQHVIVIPSSLIHFNEVIGHGCGYHGLLNDGKKIKAYKSL 1112
 QY 530 KADIASDIEEFLREACKKEPDHPVAVKLVGSLRSRAKRLIPDWILPFKRGDLH 589
 DB 1113 NR-ITDIGEVSQFLTEGILINKDFSHPMVLSLIGICLSEGS----PLVLPYMKHGDLR 1166
 QY 590 AFLASRIGENPFLPLOTILREAVDIACMEYSSNFTIRDLAANCMLAEDMTYCA 649
 DB 1167 NF-----IRNETHNPYVKDLIGFLOVAKGMKYLASKRFYRDLAARNCMUDEKFTYKVA 1221
 QY 650 DFGLSRKIVSGDY--ROGCASKLPEKMLAESLADNLVTVQSDVMAFGVYMEIMTRGO 707
 DB 1222 DFGIARDMYKEYSVYANKGAKLPYKMLAESIQOKFTTKSDVMSFGVYELMTRGA 1281
 QY 708 TPVAGINAEIVYVLGGLNFKOPPECEMEDVYDLMTCQMSADPRKRPSTCLRMELNI- 767
 DB 1282 PPYPDVTEPITVYLLQGRRLLPKPCPDLYEVMKCMKHPKAMRSPFELVSRISALF 1341
 QY 767 ---LGLSVLASADPLXINIE 785
 DB 1342 STEIGENY--HVNATYVAK 1360
 RESULT 13
 ID RON HUMAN STANDARD; PRT; 1400 AA.
 AC 004912;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (BC 2.7.1.112)
 DE (MSP RECEPTOR (P185-RON) (CDW136) (CD136 ANTIGEN).
 GN MSTIR OR RON.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KERATINOCYTES;
 RX MEDLINE; 93241719.
 RA RONSIN C., MUSCATELLI F., MATTEI M.-G., BREATHNACH R.;
 RT "A novel putative receptor protein tyrosine kinase of the met
 RT family";
 RL Oncogene 8:1195-1202(1993).
 RN [2]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RX MEDLINE; 96413302.
 RA COLLESI C., SANTORO M.M., GAUDINO G., COMOGGIO P.M.;
 RT "A splicing variant of the RON transcript induces constitutive
 RT tyrosine kinase activity and an invasive phenotype.";
 RN Mol. Cell. Biol. 16:3518-3526(1996).
 RN [3]
 RP FUNCTION.
 RX MEDLINE; 95025877.
 RA WANG M.-H., RONSIN C., GESNEL M.-C., COUPEY L., SKEEL A.,
 RA LEONARD E.J., BREATHNACH R.;
 RT "Identification of the ron gene product as the receptor for the human
 RT macrophage stimulating protein.";
 RL Science 266:117-119(1994).

CC -1- FUNCTION: RECEPTOR FOR MACROPHAGE STIMULATING PROTEIN (MSP). HAS A
 CC TIOSINE-PROTEIN KINASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC SUBUNIT: HETERODIMER FORMED OF AN ALPHA CHAIN AND A BETA
 CC CHAIN WHICH ARE DISULFIDE LINKED.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC ALTERNATIVE PRODUCTS: AN ALTERNATIVELY SPLICED FORM FOUND IN A
 CC GASTRIC CANCER CELL LINE AND CALLED DELTA-RON, LACKS PART OF THE
 CC EXTRACELLULAR DOMAIN, OLIGOMERIZE AND IS CONSTITUTIVELY ACTIVATED.
 CC -1- TISSUE SPECIFICITY: KERATINOCYTES, AND LUNG.
 CC -1- PDB: THE TWO SUBUNITS ARE PROTEOLYTICALLY DERIVED.
 CC -1- PM: PHOSPHORYLATED IN RESPONSE TO LIGAND BINDING (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE MET TYROSINE KINASE FAMILY OF RECEPTOR.
 CC -1- DATABASE: NAME-PROV; NOTE-CD guide cdm136 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdm136.htm".
 CC -----
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 CC -----
 CC EMBL: X70040; CAA49634.1;
 CC PIR: S31736; S31736.
 CC HSP: P11362; IPI.
 CC MIM: 600168;
 CC DR PRAM: P000069; Pkinase; 1.
 CC DR PRAM: P01403; Sema; 1.
 CC DR PRAM: P01437; Plectin; repeat; 1.
 CC DR PROSITE: P500107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE: P500109; PROTEIN_KINASE_TYR; 1.
 CC DR PROSITE: P550011; PROTEIN_KINASE_DOM; 1.
 CC KW Transferrase; Tyrosine-protein kinase; Receptor; Transmembrane;
 CC Glycoprotein; Signal; Phosphorylation; ATP-binding; Polymorphism;
 CC Alternative splicing.
 CC FT SIGNAL 1 24 POTENTIAL.
 CC FT CHAIN 25 1400 MACROPHAGE-STIMULATING PROTEIN RECEPTOR.
 CC FT CHAIN 25 304 MSP RECEPTOR ALPHA CHAIN (POTENTIAL).
 CC FT CHAIN 310 1400 MSP RECEPTOR BETA CHAIN (POTENTIAL).
 CC FT DOMAIN 25 957 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 958 982 POTENTIAL.
 CC FT DOMAIN 983 1400 CYTOPLASMIC (POTENTIAL).
 CC FT BINDING 1082 1345 ATP (BY SIMILARITY).
 CC FT BINDING 1086 1096 ATP (BY SIMILARITY).
 CC FT ACT_SITE 1114 1114 ATP (BY SIMILARITY).
 CC FT MOD_RES 1353 1353 BY SIMILARITY.
 CC FT MOD_RES 1360 1360 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 CC FT CARBOHYD 419 419 POTENTIAL.
 CC FT CARBOHYD 458 458 POTENTIAL.
 CC FT CARBOHYD 488 488 POTENTIAL.
 CC FT CARBOHYD 654 654 POTENTIAL.
 CC FT CARBOHYD 720 720 POTENTIAL.
 CC FT CARBOHYD 841 841 POTENTIAL.
 CC FT CARBOHYD 897 897 POTENTIAL.
 CC FT VARSLIC 322 322 MISSING (IN DELTA-RON).
 CC FT VARIANT 322 322 O -> R.
 CC FT /FTID-VAR_006350.
 CC SEQUENCE 1400 AA; 152227 MW; E132777A CRC32;
 CC -----
 CC Query Match 12.88; Score 600; DB 1; Length 1400;
 CC Best Local Similarity 27.7%; Pred. No. 1.2e-29;
 CC Matches 216; Conservative 98; Mismatches 253; Indels 212; Gaps 34;
 CC DB 80 NPACKAYOHLSGTSLSRPLPESAMSDCLAEADLQRLNSLLICRHRKRGATC 139
 CC 776 SPWCGYINSHITIGGHLTSAMHL-----VLSFHDGR--AVESRCEROLPEOOLC 824

QY 140 -LDIY-----WTVHPARSLGD-----YELDVSPEEDYTSKPMKNLSKLMK 182
 DB RLPEVYVDDPGWVAGNISANGDGAAGTLLPGFRPLPPHPPSNLVP-----LK 874
 QY 183 PDSDCLEFAM--LCTHDKDRLRKAYGEACSGIRCCRHICLAQLNSFEKKAESHAG 240
 DB 875 PE-EHAIFETIGLGAVALD--CVGINVTG-----GESCOHE-----RGD 912
 QY 241 LLCCGCP-----EDAGGGERRTIAPSCALPSVTPNCLDLRSFCRADPLCRSLMDFO 295
 DB 913 MYVCPLEPSLQLGDG-----AP-----LQVCVD-----937
 QY 296 THCHMDLIGTC-----ATROSCRLAYLGLIGTAMPNISKVNTTVALSCTCRGS-- 348
 DB 937 GECH--ILGRVVRPGDGVOSTLLGILLPL-----LVAALALALVFSYWRKOL 987
 QY 348 --GNLDECEQLERSEFSONPCLVEALNAKRFHROLFSODMASTFSVQOQNSPAMR 404
 DB 988 VLPRLAND--LASLDQTAGATPLPLIYSGSDYRSGLALPAIDGLDSTICVIGASFSDE 1046
 QY 405 AWPVYVGLVLTALYTAALAILLRKRKRETRFGQAFDSVYAKGEPAVHFRARSFNRER 464
 DB 1047 SCVP-----LIRK-----ESIQLR-----1061
 QY 465 PEREATDLSIGISDELKEDVDLIDEOQFTL--GMLCKGEGSVREAOIKOEDGSFV 522
 DB 1061 -----DLDS-----ALLAEKVDLIPHERVYTHSDVIGKHGGVYVHEGYDOANRI 1109
 QY 523 KVAVMKLRADLIASSDIEEFLEAACKKEFDHPVATKLVGSLSRAKGRPLPMTLFP 582
 DB 1110 OCAIKSL--SRITEMQVYEAFLREGLMRGNHNPVTLALIGIMLPES-----LPHVILPY 1163
 QY 583 MKHDLAFLAASIGENPNPLQLTIRIWRVADIACMEYLSNFIHRDLAARNCLAE 642
 DB 1164 MCHDDLQFIKSPQ--BNP--TWKDLISFGLQVARGMEYLAQKFEVHRLAARNCLAE 1218
 QY 643 DMTCVADDFGLSRRTYSGDY--RQGSASLTPYKWLAEADNLTYVQSDVAFCVTM 700
 DB 1219 SFTYKADDFGLARLDIREYTSVQHRHARLPVKWMLSELYTRFTKSDVWSFGVLM 1278
 QY 701 EIMRGOTPYAGIENAIYVLLIGNRLKOPRECEMEDYVILANTOCNAGADKORPSFCLR 760
 DB 1279 ELIRGAPPRPHIDPRLTHFLHAGRLRPPRYCPDSTLYVMQOCNADVAVPTFRVLV 1338
 QY 761 MELENILGQSVLSASDP--LYINI-----ERAEPYAGSLPLP--RDQYPS 806
 DB 1339 GEVQIYVALLGSHYVLPATYMWLGPSTHEMNVRECPQFS--PMPGVNVRPRLS 1394
 RESULT 14
 ID IGIR_RAT STANDARD; PRT; 1370 AA.
 AC P24062;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).
 GN IGIR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA DU J., DELAFONTAINE P.;
 RL Submitted (MAR-1994) to the EMBL/Genbank/DBD databases.
 RN [2]
 RP SEQUENCE OF 1-364 FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE; 90017496.
 RA WERNER H., WOLOSCHAK M., ADAMO M., SHEN-ORR Z., ROBERTS C.T. JR.,
 RA LEROITH D.;
 RT "Developmental regulation of the rat insulin-like growth factor I


```

RT      "cDNA cloning of mouse ret proto-oncogene and its sequence similarity
RL      to the cadherin superfamily."
CC      Oncogene 8:1087-1091(1993).
CC      -1- FUNCTION: PROBABLE RECEPTOR WITH TYROSINE-PROTEIN KINASE ACTIVITY;
CC      IMPORTANT FOR DEVELOPMENT.
CC      -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC      PROTEIN TYROSINE PHOSPHATE
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN PERIPHERAL NERVE CELLS AND
CC      HEMATOPOIETIC CELLS.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
EMBL; X67812; CAA48013.1;
LR      PIR; S29926; S29926.
DR      HSP; P11362; IAGW.
DR      MGD; MGI:97902; Ret.
DR      PFAM; PF00028; cadherin.1.
DR      PRAM; PF00068; Pkinase.1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
DR      PROSITE; PS00109; PROTEIN_KINASE_TYR.1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM.1.
KW      Transferrase; Tyrosine-protein kinase; ATP-binding; Proto-oncogene;
KM      Transmembrane; Glycoprotein; Signal.
FT      SIGNAL      1      28      POTENTIAL.
FT      CHAIN      29      1115      PROTO-ONCOGENE TYROSINE-PROTEIN KINASE
FT      DOMAIN      29      637      RECEPTOR RET.
FT      TRANSMEM      638      659      EXTRACELLULAR (POTENTIAL).
FT      DOMAIN      660      1115      CYTOPLASMIC (POTENTIAL).
FT      NP_BIND      725      1017      PROTEIN KINASE.
FT      BINDING      731      739      ATP (BY SIMILARITY).
FT      ACT_SITE      759      759      ATP (BY SIMILARITY).
FT      ACT_SITE      875      875      BY SIMILARITY.
FT      CARBOHYD      89      89      POTENTIAL.
FT      CARBOHYD      98      98      POTENTIAL.
FT      CARBOHYD      151      151      POTENTIAL.
FT      CARBOHYD      156      156      POTENTIAL.
FT      CARBOHYD      199      199      POTENTIAL.
FT      CARBOHYD      345      345      POTENTIAL.
FT      CARBOHYD      360      360      POTENTIAL.
FT      CARBOHYD      378      378      POTENTIAL.
FT      CARBOHYD      396      396      POTENTIAL.
FT      CARBOHYD      430      430      POTENTIAL.
FT      CARBOHYD      470      470      POTENTIAL.
FT      CARBOHYD      556      556      POTENTIAL.
SO      SEQUENCE      1115 AA; 123728 MW; 089A938E CRC32;

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Query Match 12.6%; Score 590.5; DB 1; Length 1115;
 Best Local Similarity 27.4%; Pred. No. 3.6e-29;
 Matches 185; Conservative 107; Mismatches 220; Indels 163; Gaps 26;

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QY      249 EDAGCGRRRTTTPSCALPSVYNCIDLRSCFADPLCRSLMD-----FQTHCHPM 301
DB      513 EEVGCPR-----SCAVNRKRECECGGSGPTGRCEWROGDGKIRNFST-CSFS 563
QY      302 DIL--STCATEQSR-----CLRAYLGLGTAMTPNFISKVNTYVALSCTCRSGNL 350
DB      564 TRCPDGHCAVERDRANICQDCLRA--DIVG-----GHE 597
QY      351 QDECEQLERSFSQNPCLVEALIAAKRFRHROLFSQWADSTFSVYQOONSFPAMRAWV-PV 409
DB      598 RGEROGIKAGYICNCFD-----EKRCFCE-----PEDSGPLCDALCRTI 639
QY      410 VLGVTALVTAAALALLLRKRKRETFGGAFFDSVMAAGEPAVHFRAARSPNRRPERIE 469

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DB      640 ITALLFSLLIISLIFCVCHHNRKHPPIASAEWTFCRPAQGFPISSSGTRRPSLD 699
QY      470 AT-----LDSLGISDELKERKEDVLIIPROQFTLGRMLGKGFEGSVREA---QLKQEDGSE 521
DB      700 STENQVDPDSKRIEDPWE-----FPKKNLYLQKTTJAEGEFEGVYATAPRLGRG-Y 753
QY      522 VKVAVKMLKADIIASSDIEELREAAKKEPDHPHVAKYVSVLSRAKGRLPIMVYLLP 581
DB      754 TVAVKYLKEN-ASQSELRDLSEFNILKQVNHVHVKLYACQSD---GPL---LLIVE 806
QY      582 FMKHDLLAFILASR-YG-----ENPN--LPLOTLRMYDIAGMEYL 623
DB      807 YAKGSLNGFLRDSRKIGPAYVSGGSRNSSLDPHERVLTMDLISFAQISRGMYL 866
QY      624 SSRNFIHDLAARNCLAEQMTVCVADRGLSRKIYSGDYKQGCASRLPYKWLLESAD 683
DB      867 AEMKLVHDLAARNILVAEGKKKISDFGLSRDYEEDSVYKSKRGRIPVKMAIESLFD 926
QY      684 NLTYVQSDVNAFGVYTMELMTRGQTPYAGIENAEIYVLLIGNRLKQPECEMEDVYDLY 743
DB      927 HYYTQSDVWSFGLVMEIYVLTGSPNPYPGIPPELFLNLKTHGMRPNDCSEMYRLML 986
QY      744 QCVSADPKQPSFTCLNRELENIIGQLSVLASQDPXYINIERAEPTAGSLELPGRDQ 803
DB      987 QCVKQEPDKRPFVADISKDEKMAVK-----SRD--YLDL----- 1020
QY      804 PYSGAGDSGGMGAVGTPSDCRYLITPGGLAEQPGQAEHQPESEPLNFORLLLLQGLLP 863
DB      1020 -----AASPSDS--LLYDGLSEE-----ETPLVDCNNAPLPRS--LP 1054
QY      864 HSCADASLKNADPN 878
DB      1055 STWLENKLYGMSDN 1069

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 Job time: 226 sec

